SEQUENCE LISTING

```
<110> Ballinger, Dennis
           Loeb, Debra
           Montgomery, Julie
           Tang, Y. Tom
           Zhou, Ping
           Goodrich, Ryle
           Liu, Chenghua
           Asundi, Vinod
           Zhao, Qing
           Wehrman, Tom
           Drmanac, Radoje
           Ren, Feiyan
           Qian, Xiahong
           Wang, Dunrui
     <120> MATERIALS AND METHODS RELATING TO LIPID METABOLISM
     <130> 28110/35915A
W. T.
     <150> US 60/197,137
     <151>
            2000-04-14
M
[1]
     <150> US 09/714,936
            2000-11-17
     <151>
U
T)
     <150> US 09/667,298
<151> 2000-09-22
ű.
     <150>
            US 09/631,451
<151>
            2000-08-03
     <150> US 09/598,042
     <151>
            2000-06-20
. Es
     <160> 45
     <170> PatentIn version 3.0
     <210>
            1
     <211> 1858
     <212> DNA
     <213> Homo sapiens
     <220>
     <221> CDS
     <222> (46)..(1143)
     <220>
     <221> misc_feature
     <222> (46) ... (1143)
     <223> n = a or c or g or t
     <400> 1
     cccacgcgtc cgggcctccc tccacctgtc ttctcagagc agata atg gca agc atg
                                                                           57
                                                       Met Ala Ser Met
     gct gcc gtg ctc acc tgg gct ctg gct ctt ctt tca gcg ttt tcg gcc
                                                                          105
     Ala Ala Val Leu Thr Trp Ala Leu Ala Leu Leu Ser Ala Phe Ser Ala
                         10
```

							ttc Phe										153
							cag Gln										201
							agc Ser										249
	aag Lys	ttc Phe 70	ctg Leu	gaa Glu	aag Lys	ctg Leu	agg Arg 75	cct Pro	ctg Leu	agt Ser	Gly ggg	agc Ser 80	gag Glu	gct Ala	cct Pro	cgg Arg	297
							ggc Gly										345
							ctc Leu										393
thus the tens to the their their their							gag Glu										441
Ţ1							cag Gln										489
							999 Gly 155										537
division of the second							gct Ala										585
							ttc Phe										633
							Gly 999										681
							gcc Ala										729
							ctc Leu 235										777
							gac Asp										825
							gag Glu										873

ctc tcc gag gag gtg cgc cag cga ctt cag gct ttc cgc cag gac acc Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe Arg Gln Asp Thr 280 . 285 . 290	921
tac ctg cag ata gct gcc ttc act cgc gcc atc gac cag gag act gag Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp Gln Glu Thr Glu 295 300 305	969
gag gtc cag cag cag ctg gcg cca cct cca cca ggc cac agt gcc ttc Glu Val Gln Gln Leu Ala Pro Pro Pro Pro Gly His Ser Ala Phe 310 315 320	1017
gcc cca gag ttt caa caa aca gac agt ggc aag gtt ctg agc aag ctg Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val Leu Ser Lys Leu 325 330 335 340	1065
cag gcc cgt ctg gat gac ctg tgg gaa gac atc act cac agc ctt cat Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp Ile Thr His Ser Leu His 345 350 355	1113
gac cag ggc cac agc cat ctg ggg gac ccc tgaggatcta cctgcccagg Asp Gln Gly His Ser His Leu Gly Asp Pro 360 365	1163
cccattccca geteettgte tggggageet tggetetgag eetetageat ggtteagtee	1223
ttgaaagtgg cctgttgggt ggagggtgga aggtcctgtg caggacaggg aggccaccaa	1283
aggggctgct gtctcctgca tatccagcct cctgcgactc cccaatctgg atgcattaca	1343
ttcaccaggc tttgcaaacc cagcctccca gtgctcattt gggaatgctc atgagttact	1403
ccattcaagg gtgagggagt agggagggag aggcaccatg catgtgggtg attatctgca	1463
agectgtttg ccgtgatgct ggaagcctgt gccactacat cctggagttt ggctctagtc	1523
acttetgget geetggtgge eactgetaca getggteeae agagaggage acttgtetee	1583
ccagggctgc catggcagct atcaggggaa tagaagggag aaagagaata tcatggggag	1643
aacatgtgat ggtgtgtgaa tatccctgct ggctctgatg ctggtgggta cgaaaggtgt	1703
gggctgggat aagagagggc agagcccatg ttttctgaca taactctaca cctanataag	1763
ggactgaacc cttccaactg cgggagctcc ttaaaccctt ctggggagca tactgggggc	1823
tottoeccat ottoagooco ttoototggg ttoec	1858
<210> 2 <211> 366 <212> PRT <213> Homo sapiens	
<220> <221> misc_feature <222> (46)(1143) <223> n = a or c or g or t	
<400> 2	

Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala Leu Ala Leu Leu Ser 1 10 15

Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr Phe Ser 20 25 30

Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys 35 40 45

Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu 50 55 60

Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser Gly Ser 65 70 75 80

Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu 85 90 95

Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala 100 105 110

Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln
115 120 125

Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val 130 135 140

Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala 145 150 155 160

Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu 165 170 175

Gln Ser Arg Val Val His His Thr Gly Arg Phe Lys Glu Leu Phe His 180 185 190

Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu 195 200 205

Leu His Arg Ser Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu 210 215 220

Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys 225 230 235 240

Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg Glu Glu 245 250 255

Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Gly Pro 260 265 270

275 280 285	
Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp 290 295 300	
Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala Pro Pro Pro Pro Gly 305 310 315 320	
His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val 325 330 335 .	
Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp Ile Thr 340 345 350	
His Ser Leu His Asp Gln Gly His Ser His Leu Gly Asp Pro 355 360 365	
<210> 3 <211> 1425 <212> DNA <213> Homo sapiens	
<220> <221> CDS <222> (181)(1146)	
(2222 (101)(1140)	
<400> 3 gccaggagcc atgtgggttt ttctaggaac caaaatcact tcccggaatt gaccaactgg	60
<400> 3	60 120
<400> 3 gccaggagcc atgtgggttt ttctaggaac caaaatcact teeeggaatt gaccaactgg	
<pre><400> 3 gccaggagcc atgtgggttt ttctaggaac caaaatcact tcccggaatt gaccaactgg tagactcgcc tagaggggaa gcattgtgtc ctagttgagg ctaacagtca gtatccagcc</pre>	120
<pre><400> 3 gccaggagcc atgtgggttt ttctaggaac caaaatcact tcccggaatt gaccaactgg tagactcgcc tagaggggaa gcattgtgtc ctagttgagg ctaacagtca gtatccagcc tcaacattca gcagaggccc cagatcagcg tctgagccag gccaacaatg accaaggagg atg gga tcc tgg gtg cag ctc atc aca agc gtc ggg gtg cag caa aac Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn</pre>	120
<pre><400> 3 gccaggagcc atgtgggttt ttctaggaac caaaatcact tcccggaatt gaccaactgg tagactcgcc tagaggggaa gcattgtgtc ctagttgagg ctaacagtca gtatccagcc tcaacattca gcagaggccc cagatcagcg tctgagccag gccaacaatg accaaggagg atg gga tcc tgg gtg cag ctc atc aca agc gtc ggg gtg cag caa aac Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn 1</pre>	120 180 228
cagagage atgtgggtt ttetaggaac caaaatcact teeeggaatt gaccaactgg tagactegee tagaggggaa geattgtgte etagttgagg etaacagtea gtatecagee teaacattea geagaggee cagateageg tetgageeag geeaacaatg accaaggagg atg gga tee tgg gtg cag eta atc aca age gte ggg gtg cag eaa aac Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn 1 5 10 15 cat cea gge tgg aca gtg get gga eag tte eaa gaa aag aaa ege tte His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe 20 25 30 act gaa gaa gte att gaa tae tte eag aag aaa gtt age eea gtg eat Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His	120 180 228 276
cagagagcc atgtgggttt ttctaggaac caaaatcact tcccggaatt gaccaactgg tagactcgcc tagaggggaa gcattgtgtc ctagttgagg ctaacagtca gtatccagcc tcaacattca gcagaggccc cagatcagcg tctgagccag gccaacaatg accaaggagg atg gga tcc tgg gtg cag ctc atc aca agc gtc ggg gtg cag caa aac Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn 1 5 10 15 cat cca ggc tgg aca gtg gct gga cag ttc caa gaa aag aaa cgc ttc His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe 20 25 30 act gaa gaa gtc att gaa tac ttc cag aag aaa gtt agc cca gtg cat Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His 35 40 45 ctg aaa atc ctg ctg act agc gat gaa gcc tgg aag aga ttc gtg cgt Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg	120 180 228 276

85 90 95 aaa gaa cag cag ttt agg gag tgg ttt ttg aaa gag ttt cct caa atc 516 Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile 105 110 aga tgg aag att cag gag tcc ata gaa agg ctt cgt gtc att gca aat 564 Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn 115 120 gag att gaa aag gtc cac aga ggc tgc gtc atc gcc aat gtg gtg tct 612 Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser 135 ggc tcc act ggc atc ctg tct gtc att ggc gtt atg ttg gca cca ttt 660 Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe 150 155 aca gca ggg ctg agc ctg agc att act gca gct ggg gta ggg ctg gga 708 Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly 165 170 ata gca tct gcc acg gct ggg atc gcc tcc agc atc gtg gag aac aca 756 Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr 180 185 190 tac aca agg tca gca gaa ctc aca gcc agc agg ctg act gca acc agc 804 Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser 195 200 act gac caa ttg gag gca tta agg gac att ctg cat gac atc aca ccc 852 Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro 210 215 220 aat gtg ctt tcc ttt gca ctt gat ttt gac gaa gcc aca aaa atg att 900 Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile 230 gcg aat gat gtc cat aca ctc agg aga tet aaa gcc act gtt gga cgc 948 Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg 245 250 255 cct ttg att gct tgg cga tat gta cct ata aat gtt gtt gag aca ctg 996 Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu aga aca egt ggg gee eee ace egg ata gtg aga aaa gta gee egg aac 1044 Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn 280 ctg ggc aag gcc act tca ggt gtc ctt gtt gtg ctg gat gta gtc aac 1092 Leu Gly Lys Ala Thr Ser Gly Val Leu Val Leu Asp Val Val Asn 295 300 ctt gtg caa gac tca ctg gac ttg cac aag ggg gca aaa tcc gag tct 1140 Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser 310 315 gct gag tcgctgaggc agtgggctca ggagctggag gagaatctca atgagctcac 1196 Ala Glu ccatatccat cagagtctaa aagcaggcta ggcccaattg ttqcgggaag tcagggaccc

caaacggagg	gactggctga	agccatggca	gaagaacgtg	gattgtgaag	atttcatgga	1316
catttattag	ttccccaaat	taatactttt	ataatttcct	atgcctgtct	ttaccgcaat	1376
ctctaaacac	caattgtgaa	gatttcatgg	acacttatca	cttccccaa		1425

<210> 4 <211> 322 <212> PRT <213> Homo sapiens

<400> 4

Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn 1 5 10 15

His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe 20 25 30

Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His 35 40 45

Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg 50 55 60

Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu 65 70 75 80

Lys Asn Leu Thr Pro Tyr Val Ala Ile Glu Asp Lys Asp Met Gln Gln 85 90 95

Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile
100 105 110

Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn 115 120 125

Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser 130 135 140

Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe 145 150 155 160

Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly 165 170 175

Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr 180 185 190

Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser

205

200

195

Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro 210 215 Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg 250 Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn 280 41 a Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn U 41 Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser 4] 310 315 O £ Ala Glu Ŧ: -1 <210> 5 (T <211> 1931 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (18)..(452) gaagettete gaggace atg gaa ett gea etg etg tgt ggg etg gtg 50 Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val atg gct ggt gtg att cca atc cag ggc ggg atc ctg aac ctg aac aag Met Ala Gly Val Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys 98 15 atg gtc aag caa gtg act ggg aaa atg ccc atc ctc tcc tac tgg ccc 146 Met Val Lys Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro 30 tac ggc tgt cac tgc gga cta ggt ggc aga ggc caa ccc aaa gat gcc 194 Tyr Gly Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala 45

acg gac tgg tgc tgc cag acc cat gac tgc tgc tat gac cac ctg aag

Thr Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys

70 75 60 65 290 acc cag ggg tgc ggc atc tac aag gac tat tac aga tac aac ttt tcc Thr Gln Gly Cys Gly Ile Tyr Lys Asp Tyr Tyr Arg Tyr Asn Phe Ser 338 cag ggg aac atc cac tgc tct gac aag gga agc tgg tgt gag cag cag Gln Gly Asn Ile His Cys Ser Asp Lys Gly Ser Trp Cys Glu Gln Gln ctg tgt gcc tgt gac aag gag gtg gcc ttc tgc ctg aag cgc aac ctg 386 Leu Cys Ala Cys Asp Lys Glu Val Ala Phe Cys Leu Lys Arg Asn Leu 110 115 gae ace tae cag aag ega etg egt tte tae tgg egg eee cae tge egg 434 Asp Thr Tyr Gln Lys Arg Leu Arg Phe Tyr Trp Arg Pro His Cys Arg ggg cag acc cct ggg tgc tagaagccca caccctctac cctgttcctc 482 Gly Gln Thr Pro Gly Cys 140 agcatggage tetggeatee ceaceteagt atetaacetg aaccageetg getttteaaa 542 cacteegggg ggaggtagte ceageeteee eeggaaceet etaceaatge ettetgaeet 602 tctgaagctt tccgaatcct cccagttgag gcagtagctg tgtcctctga gggtggatgg 662 722 gaatettggg agaageecaa geaagggage ceteagaggt ggtgtttgga eeaaageate ggggtggggg aggggtetge egetgteece caectgetgg ecceettgte etteeteace 782 ccctccaata tagtctcgga gctacaaccg cagcagccac tataaagggc aatattgatc 842 902 tttctgtcca tgtggctcta tcttttaaaa cctcaaggcc ctccactgtc ctaagataaa 962 gcctctcata ggcactgggg accctgcaca gtctggccat gtgaccctct ccccaggcaa gctctgaagt ccctgcaggt ggaggccatg cctgtcttaa actcagttgc atccctggtg 1022 1082 cccaaagcaa caccagaacc aagaaggagc tccataaatc cttcttgggt gaagcctaga caaagccgcc aggtcttgtg gctccaggca ccagagcctt gagtactttc tcctgcctcc 1142 1202 aggcattggc tcagggtgaa ttacaagggg ctactgaatg gctattactt tcatcacgac tgatececae etecteaggg teaaaggget actttetgga agteteeca ggetgaetee 1262 ttotocotga otgoaagggo toactocoto otocaagoto coacaatgot toatggotot 1322 1382 gccgcttacc tagcttggcc tagagtggca aatggaactt ctctgatctc ccccaactag actggagccc ccgaaggatg gagaccatgt ctgtgccatc tctgtttccc ctgttttccc 1442 acatactagg tgctcaattc atgcctgtga atggcgtgag cccataatgg atacacagag 1502 1562 gttgcagcag atggtgtggg tacctcaccc agatatette caggeccaag geceetetee ctgagtgagg ccaggtgttg gcagccaact gctccaatct gcctccttcc cctaaatact 1622 geoetggtet agtgggaget geetteeeee tgeeceaeet eteceaeeaa gaggeeaeet 1682 gtcactcatg gccaggagag tgacaccatg gagggtacaa ttgccagctc ccccgtgtct 1742 gtgcagcatt gtctgggttg aatgacactc tcaaattgtt cctgggatcg ggctgaggcc 1802 aggestates tggaaceace tetetgettg gtetgacees ttggestate cagtttteet 1862 ggttccctca caggtttctc cagaaagtac tccctcagta aagcatttgc acaagaaaaa 1922 1931 aaaaaaaa

<210> 6

<211> 145

<212> PRT

<213> Homo sapiens

<400> 6

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val Ile 5

Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys Gln Val

Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly Cys His Cys

Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr Asp Trp Cys Cys

Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys Thr Gln Gly Cys Gly

Ile Tyr Lys Asp Tyr Tyr Arg Tyr Asn Phe Ser Gln Gly Asn Ile His

Cys Ser Asp Lys Gly Ser Trp Cys Glu Gln Gln Leu Cys Ala Cys Asp

Lys Glu Val Ala Phe Cys Leu Lys Arg Asn Leu Asp Thr Tyr Gln Lys

Arg Leu Arg Phe Tyr Trp Arg Pro His Cys Arg Gly Gln Thr Pro Gly 135

Cys 145

<210> 7

<211> 1840

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (140) .. (1840)

<400> 7 tcccgggtcg acgatttctt cctgatccca cagcatcgca gagctcggga ggcacagctc 60 acaqacacaq qaaacacaqq actqctattc tqctctcctq cccacqqtqa tctqqtqcca 120 gctggtggaa cagtgggtg atg gcg tcc ctg ctg caa gac cag ctg acc act 172 Met Ala Ser Leu Leu Gln Asp Gln Leu Thr Thr gat cag gac ttg ctg ctg atg cag gaa ggc atg ccg atg cgc aag gtg 220 Asp Gln Asp Leu Leu Met Gln Glu Gly Met Pro Met Arg Lys Val agg tcc aaa agc tgg aag aag cta aga tac ttc aga ctt cag aat gac 268 Arg Ser Lys Ser Trp Lys Lys Leu Arg Tyr Phe Arg Leu Gln Asn Asp 30 gge atg aca gte tgg cat gea egg cag gee agg gge agt gee aag eee 316 Gly Met Thr Val Trp His Ala Arg Gln Ala Arg Gly Ser Ala Lys Pro age tte tea ate tet gat gtg gag aca ata egt aat gge eat gat tee 364 Ser Phe Ser Ile Ser Asp Val Glu Thr Ile Arg Asn Gly His Asp Ser gag ttg ctg cgt agc ctg gca gag gag ctc ccc ctg gag cag ggc ttc 412 Glu Leu Leu Arg Ser Leu Ala Glu Glu Leu Pro Leu Glu Gln Gly Phe acc att gtc ttc cat ggc cgc cgc tcc aac ctg gac ctg atg gcc aac 460 Thr Ile Val Phe His Gly Arg Arg Ser Asn Leu Asp Leu Met Ala Asn agt gtt gag gag gcc cag ata tgg atg cga ggg ctc cag ctg ttg gtg 508 Ser Val Glu Glu Ala Gln Ile Trp Met Arg Gly Leu Gln Leu Leu Val 11.5 gat ctt gtc acc agc atg gac cat cag gag cgc ctg gac caa tgg ctg 556 Asp Leu Val Thr Ser Met Asp His Gln Glu Arg Leu Asp Gln Trp Leu 130 age gat tgg ttt caa cgt gga gae aaa aat cag gat ggt aag atg agt 604 Ser Asp Trp Phe Gln Arg Gly Asp Lys Asn Gln Asp Gly Lys Met Ser ttc caa gaa gtt cag cgg tta ttg cac cta atg aat gtg gaa atg gac 652 Phe Gln Glu Val Gln Arg Leu Leu His Leu Met Asn Val Glu Met Asp caa gaa tat gcc ttc agt ctt ttt cag gca gca gac acg tcc cag tct 700 Gln Glu Tyr Ala Phe Ser Leu Phe Gln Ala Ala Asp Thr Ser Gln Ser gga acc ctg gaa gga gaa gaa ttc gta cag ttc tat aag gca ttg act 748 Gly Thr Leu Glu Gly Glu Glu Phe Val Gln Phe Tyr Lys Ala Leu Thr 190 195 aaa cgt gct gag gtg cag gaa ctg ttt gaa agt ttt tca gct gat ggg 796 Lys Arg Ala Glu Val Gln Glu Leu Phe Glu Ser Phe Ser Ala Asp Gly 210

				ctg Leu 225										844
_	~ ~	_	_	 acc Thr		-		_		-		_	-	892
				agt Ser										940
			_	ctc Leu	_		_	_						988
				tat Tyr										1036
				cat His 305										1084
				gag Glu										1132
				gat Asp										1180
				acc Thr										1228
				cag Gln										1276
				acc Thr 385										1324
				gag Glu										1372
_	_			 ccc Pro		_	_		_		 ,			1420
				aag Lys										1468
				gaa Glu										1516
				ttt Phe 465										1564

				aag Lys													1612
				tcc Ser 495													1660
				tca Ser													1708
				aag Lys													1756
				aat Asn													1804
				tct Ser													1840
are that their traditions that their	<210 <211 <212 <213	L> 5 2> I 3> I		sapi	iens												
	< 400)> {	3														
ir. ii di dinar				Leu	Leu 5	Gln	Asp	Gln	Leu	Thr 10	Thr	Asp	Gln	Asp	Leu 15	Leu	
R. Tang may R. R. R. R. Radi	Met 1	Ala	Ser	Leu Glu 20	5		_			10					15		
It	Met 1 Leu	Ala Met	Ser	Glu	5 Gly	Met	Pro	Met	Arg 25	10 Lys	Val	Arg	Ser	Lys 30	15 Ser	Trp	
It	Met 1 Leu Lys	Ala Met Lys	Ser Gln Leu 35	Glu 20	5 Gly Tyr	Met Phe	Pro	Met Leu 40	Arg 25 Gln	10 Lys Asn	Val Asp	Arg Gly	Ser Met 45	Lys 30 Thr	15 Ser Val	Trp	
It	Met 1 Leu Lys	Ala Met Lys Ala	Gln Leu 35 Arg	Glu 20 Arg	5 Gly Tyr Ala	Met Phe Arg	Pro Arg Gly 55	Met Leu 40 Ser	Arg 25 Gln Ala	Lys Asn	Val Asp Pro	Arg Gly Ser	Ser Met 45 Phe	Lys 30 Thr	15 Ser Val	Trp Trp Ser	
It	Met 1 Leu Lys His Asp	Ala Met Lys Ala 50	Gln Leu 35 Arg	Glu 20 Arg	5 Gly Tyr Ala Ile	Met Phe Arg Arg	Pro Arg Gly 55 Asn	Met Leu 40 Ser	Arg 25 Gln Ala His	Lys Asn Lys	Val Asp Pro Ser 75	Arg Gly Ser 60	Ser Met 45 Phe	Lys 30 Thr Ser	Ser Val Ile	Trp Trp Ser Ser	
It	Met 1 Leu Lys His Asp 65	Ala Met Lys Ala 50 Val	Gln Leu 35 Arg Glu	Glu 20 Arg Gln Thr	Gly Tyr Ala Ile Leu 85	Met Phe Arg Arg 70 Pro	Pro Arg Gly 55 Asn	Met Leu 40 Ser Gly	Arg 25 Gln Ala His	Lys Asn Lys Asp Gly 90	Val Asp Pro Ser 75	Arg Gly Ser 60 Glu	Ser Met 45 Phe Leu	Lys 30 Thr Ser Leu Val	Ser Val Ile Arg	Trp Trp Ser Ser 80	

Met Asp His Gln Glu Arg Leu Asp Gln Trp Leu Ser Asp Trp Phe Gln 130 135 140

Arg Gly Asp Lys Asn Gln Asp Gly Lys Met Ser Phe Gln Glu Val Gln 145 150 155 160

Arg Leu Leu His Leu Met Asn Val Glu Met Asp Gln Glu Tyr Ala Phe 165 170 175

Ser Leu Phe Gln Ala Ala Asp Thr Ser Gln Ser Gly Thr Leu Glu Gly 180 185 190

Glu Glu Phe Val Gln Phe Tyr Lys Ala Leu Thr Lys Arg Ala Glu Val 195 200 205

Gln Glu Leu Phe Glu Ser Phe Ser Ala Asp Gly Gln Lys Leu Thr Leu 210 215 220

Leu Glu Phe Leu Asp Phe Leu Gln Glu Glu Gln Lys Glu Arg Asp Cys 235 230 235

Thr Ser Glu Leu Ala Leu Glu Leu Ile Asp Arg Tyr Glu Pro Ser Asp 245 250 255

Ser Gly Lys Leu Arg His Val Pro Ser Met Asp Gly Phe Leu Ser Tyr 260 265 270

Leu Cys Ser Lys Asp Gly Asp Ile Phe Asn Pro Ala Cys Leu Pro Ile 275 280 285

Tyr Gln Asp Met Thr Gln Pro Leu Asn His Tyr Phe Ile Cys Ser Ser 290 295 300

His Asn Thr Tyr Leu Val Gly Asp Gln Leu Cys Gly Gln Ser Ser Val 305 310 315 320

Glu Gly Tyr Ile Arg Ala Leu Lys Arg Gly Cys Arg Cys Vai Glu Val 325 330 335

Asp Val Trp Asp Gly Pro Ser Gly Glu Pro Val Val Tyr His Gly His
340 345 350

Thr Leu Thr Ser Arg Ile Leu Phe Lys Asp Val Val Ala Thr Val Ala 355 360 365

Gln Tyr Ala Phe Gln Thr Ser Asp Tyr Pro Val Ile Leu Ser Leu Glu 370 375 380

Thr His Cys Ser Trp Glu Gln Gln Thr Met Ala Arg His Leu Thr 390 385 Glu Ile Leu Gly Glu Gln Leu Leu Ser Thr Thr Leu Asp Gly Val Leu Pro Thr Gln Leu Pro Ser Pro Glu Glu Leu Arg Arg Lys Ile Leu Val 425 Lys Gly Lys Lys Leu Thr Leu Glu Glu Asp Leu Glu Tyr Glu Glu Glu 435 Glu Ala Glu Pro Glu Leu Glu Glu Ser Glu Leu Ala Leu Glu Ser Gln 450 Phe Glu Thr Glu Pro Glu Pro Gln Glu Gln Asn Leu Gln Asn Lys Asp 470 465 Lys Lys Lys Lys Ser Lys Pro Ile Leu Cys Pro Ala Leu Ser Ser Leu 495 485 Val Ile Tyr Leu Lys Ser Val Ser Phe Arg Ser Phe Thr His Ser Lys 505 500 Glu His Tyr His Phe Tyr Glu Ile Ser Ser Phe Ser Glu Thr Lys Ala 520 515 Lys Arg Leu Ile Lys Glu Ala Gly Asn Glu Phe Val Gln His Asn Thr 535 530 Arg Gln Leu Ser Arg Val Tyr Pro Ser Gly Leu Arg Thr Gly Ser Ser 555 550 545 Ile Tyr Asn Pro Gln Gly Tyr 565 <210> 9 <211> 1384 <212> DNA <213> Homo sapiens <400> 9 ccaactaagc ttgcctaatt tgcttcagaa ttggaagagg gaattgcagc aggaaaatat 60 gtgaagagtt tttaaaccca caaattcttc ttactttaga attagttgtt acattggcag 120 gaaaaaataa atgcagatgt tggaccatgt tggaaacctt gtcaagacag tggattgtct 180 cacacagaat ggaaatgtgg cttctgattc tggtggcgta tatgttccag agaaatgtga 240

attcagtaca tatgccaact aaagctgtgg acccagaagc attcatgaat attagtgaaa

tcatccaaca tcaaggctat ccctgtgagg aatatgaagt cgcaactgaa gatgggtata	360
tcctttctgt taacaggatt cctcgaggcc tagtgcaacc taagaagaca ggttccaggc	420
ctgtggtgtt actgcagcat ggcctagttg gaggtgctag caactggatt tccaacctgc	480
ccaacaatag cctgggcttc attctggcag atgctggttt tgacgtgtgg atggggaaca	540
gcaggggaaa cgcctggtct cgaaaacaca agacactctc catagaccaa gatgagttct	600
gggctttcag ttatgatgag atggctaggt ttgaccttcc tgcagtgata aactttattt	660
tgcagaaaac gggccaggaa aagatctatt atgtcggcta ttcacagggc accaccatgg	720
getttattge attttecace atgecagage tggeteagaa aateaaaatg tattttgett	780
tagcacccat agecactgtt aagcatgcaa aaagccccgg gaccaaattt ttgttgctgc	840
cagatatgat gatcaaggga ttgtttggca aaaaagaatt tctgtatcag accagatttc	900
tcagacaact tgttatttac ctttgtggcc aggtgattct tgatcagatt tgtagtaata	960
tcatgttact tctgggtgga ttcaacacca acaatatgaa catgagccga gcaagtgtat	1020
atgctgccca cactettgct ggaacatetg tgcaaaatat tetacaetgg agecaggcag	1080
tgaattetgg tgaacteegg geatttgaet gggggagtga gaccaaaaat etggaaaaat	1140
gcaatcagcc aacteetgta aggtacagag teagagatat gaeggteeet acagcaatgt	1200
ggacaggagg tcaggactgg ctttcaaatc cagaagacgt gaaaatgctg ctctctgagg	1260
tgaccaacct catctaccat aagaatattc ctgaatgggc tcatgtggat ttcatctggg	1320
gtttggatgc tcctcaccgt atgtacaatg aaatcatcca tctgatgcag caggaggaga	1380
ccat	1384
<210> 10 <211> 1915 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (180)(1046)	
<pre><400> 10 ccgcacgagg gaaagaacat taggaatgcc ttttagtgcc ttgcttcctg aactagctca</pre>	60
cagtageceg geggeecagg geaateegae eacattteae teteaeeget gtaggaatee	120
agatgcaggc caagtacagc agcacgaggg acatgctgga tgatgatggg gacaccacc	179
atg age etg cat tet caa gee tet gee aca act egg cat eea gag eee Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro 1 5 10 15	227
cgg cgc aca gag cac agg gct ccc tct tca acg tgg cga cca ytg gcc Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala 20 25 30	275

	ctg Leu	acc Thr	ctg Leu 35	ctg Leu	act Thr	ttg Leu	tgc Cys	ttg Leu 40	gtg Val	ctg Leu	ctg Leu	ata Ile	999 Gly 45	ctg Leu	gca Ala	gcc Ala	:	323
									tac Tyr								:	371
									aga Arg								4	419
									ata Ile								4	467
									gag Glu 105								!	515
			_		_			_	tct Ser	-				_			!	563
Joseph Marie State Marie									gca Ala								(611
									gga Gly								•	659
									tgt Cys								•	707
THE STATE OF THE S				_	_	_			aaa Lys 185		_	_	_	_		-	•	755
									ttc Phe								;	803
									tgg Trp								;	851
									ata Ile								;	899
									aat Asn									947
									tgt Cys 265								!	995
									cct Pro								1:	043

tga ttcgcc	ctct gcaacta	acaa atagcag	gagt gagccag	ggcg gtgccaa	aagc	1096
aagggctagt	tgagacattg	ggaaatggaa	cataatcagg	aaagactatc	tctctgacta	1156
gtacaaaatg	ggttctcgtg	tttcctgttc	aggatcacca	gcatttctga	gcttgggttt	1216
atgcacgtat	ttaacagtca	caagaagtct	tatttacatg	ccaccaacca	acctcagaaa	1276
cccataatgt	catctgcctt	cttggcttag	agataacttt	tagctctctt	tcttctcaat	1336
gtctaatatc	acctccctgt	tttcatgtct	tccttacact	tggtggaata	agaaactttt	1396
tgaagtagag	gaáatacatt	gaggtaacat	ccttttctct	gacagtcaag	tagtccatca	1456
gaaattggca	gtcacttccc	agattgtacc	agcaaataca	caaggaattc	tttttgtttg	1516
tttcagttca	tactagtccc	ttcccaatcc	atcagtaaag	accccatctg	ccttgtccat	1576
gccgtttccc	aacagggatg	tcacttgata	tgagaatctc	aaatctcaat	gccttataag	1636
cattccttcc	tgtgtccatt	aagactctga	taattgtctc	ccctccatag	gaatttctcc	1696
caggaaagaa	atatatcccc	atctccgttt	catatcagaa	ctaccgtccc	cgatattccc	1756
ttcagagaga	ttaaagacca	gaaaaaaggg	gggcttttt	tttgcacctg	taatagtttc	1816
cggtcctttt	ttttttcctt	gacccctttt	ttttcccttc	cgggggtgga	gggtttatta	1876
taattaaagg	gaataccggg	gaaaaaaaaa	aaaaagggg			1915

<210> 11 <211> 288 <212> PRT

<213> Homo sapiens

<400> 11

Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro 1 5 10 15

Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala 20 25 30

Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala 35 40 45

Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln 50 60

Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu 65 70 75 80

Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln 85 90 95

His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Gly

Q)

man pan

41

4)

į.

<220> <221> CDS

<222> (200)..(2395)

<223> Xaa = Unknown or other

Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser Leu Arg 120 115 Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys Ser Pro 130 Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr 150 145 Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala 185 180 Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu 200 Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro . 220 215 Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp 245 250 Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val 260 Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp 285 275 <210> 12 <211> 2420 <212> DNA <213> Homo sapiens <220> <221> misc feature $\langle 223 \rangle$ n = a or c or g or t

< 400)	12														
	-		ggaaq	ggaga	aa gg	gcgga	aatgt	999	gagg	gctc	aggg	gggat	gt q	gggag	gggacg	60
aac	ggaga	aag (3999	agaga	ag gg	ggggt	ccag	g tct	ccc	ctgg	ccga	agcat	ctt 1	tttt	ttttg	120
gaag	gtcct	ag (gacta	aatci	cc ca	aggad	ccago	e act	ctto	ctcc	cago	ccct	ag q	ggtc	ctgctc	180
ggc	caagg	gcc	ttcc	etge	-	-		_	-			-		_	c ccc c Pro	232
		_	_	-	-	_	_	_	agt Ser	_	_				_	280
									gcc Ala							328
									ccc Pro							376
									atc Ile							424
									gag Glu 85							472
									ggc Gly							520
	_	_		_	_	_	_		acc Thr	-	_	_			_	568
									gac Asp							616
									ctc Leu							664
									caa Gln 165							712
_		_	_				-	_	ccc Pro	_			_			760
_		_	_				_		tgg Trp	_			_	_		808
									gtc Val							856

			gtc Val 225									904
			ttt Phe									952
			ctc Leu									1000
			ggg Gly									1048
	-	_	gca Ala				_	_	-		 _	1096
_	_	 	gtc Val 305	_	_					 _		1144
			gaa Glu									1192
			gac Asp									1240
			gct Ala									1288
_	 _	 _	atc Ile		_	_	_		_		 _	1336
			aag Lys 385	_			_			_	 _	1384
			gat Asp									1432
			gtc Val									1480
			caa Gln									1528
			cgc Arg									1576
			gtg Val 465									1624

aac cac ggc ctg cag gag acc tgg tac tgg gac tct ggg aat ata aca Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly Asn Ile Thr

				_				_	_			act Thr		~		_	1720
٠												tgc Cys					1768
												gca Ala 535					1816
												atc Ile					1864
												tgc Cys					1912
Port Ann gran greek fores												cgt Arg					1960
the stands of th												ttc Phe					2008
Hard Balle all												999 Gly 615					2056
State of the state												cca Pro					2104
												gaa Glu					2152
												aac Asn					2200
	ggc Gly	atc Ile	act Thr 670	gtg Val	ggd Xaa	tgc Cys	tgg Trp	gat Asp 675	ctc Leu	tac Tyr	cgg Arg	cat His	gac Asp 680	att Ile	gac Asp	tgt Cys	2248
												aac Asn 695					2296
												agb Xaa					2344
												cat His					2392

cac macttgccac attggtgatg ccttc His

<210> 13 <211> 732

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature <223> n = a or c or g or t

<400> 13

Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu

Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly 20

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly 40 35

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly 50

Glu Trp Gly Thr Ile Cys Asp Asp Phe Thr Leu Gln Ala Ala His

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His 90

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu 100

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys 135

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val 150

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly 170 165

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg 185 180

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His

Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg 210 215 220

Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser 225 230 235 240

Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser 245 250 255

Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro 260 265 270

Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala 275 280 285

Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu 290 295 300

Val Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val 305 310 315 320

Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Tyr Arg Lys Trp 325 330 335

Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser 340 345 350

Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala 355 360 365

Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp 370 375 380

Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln 385 390 395 400

Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg

Val Ile His Ser Val Ser Leu Gln Ile Arg Leu Ser Gly Gly Arg Ser 420 425 430

Gln His Glu Gly Arg Val Glu Val Gln Ile Gly Gly Pro Gly Pro Leu 435 440 445

Arg Trp Gly Leu Ile Cys Gly Asp Asp Trp Gly Thr Leu Glu Ala Met 450 455 460

Val Ala Cys Arg Gln Leu Gly Leu Gly Tyr Ala Asn His Gly Leu Gln 465 470 475 480

Gly Val Arg Cys Thr Gly Thr Glu Leu Ser Leu Asp Gln Cys Ala His 500 505 510

His Gly Thr His Ile Thr Cys Lys Arg Thr Gly Thr Arg Phe Thr Ala 515 520 525

Gly Val Ile Cys Ser Glu Ala Ser Asp Leu Leu Leu His Ser Ala Leu 530 535 540

Val Gln Glu Thr Ala Tyr Ile Glu Asp Arg Pro Leu His Met Leu Tyr 545 550 555 560

Cys Ala Ala Glu Glu Asn Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn 565 570 575

Trp Pro Tyr Gly His Arg Arg Leu Leu Arg Phe Cys Ser Gln Ile His 580 585 590

Asn Leu Gly Arg Ala Asp Phe Arg Pro Lys Ala Gly Arg His Ser Trp 595 600 605

Val Trp His Glu Cys His Gly His Tyr His Ser Thr Asp Phe Phe Thr 610 615 620

His Tyr Asp Ile Leu Thr Pro Xaa Gly Thr Lys Val Ala Glu Gly His 625 630 635 640

Lys Ala Ser Phe Cys Leu Glu Asp Thr Glu Cys Gln Glu Asp Val Ser 645 650 655

Lys Arg Tyr Glu Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Val Xaa 660 665 670

Cys Trp Asp Leu Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile 675 680 685

Thr Asp Val Lys Pro Gly Asn Tyr Ile Leu Gln Val Val Ile Asn Pro 690 695 700

Asn Phe Glu Val Ala Glu Xaa Asp Phe Thr Asn Asn Ala Met Lys Cys 705 710 715 720

	Asn	Cys	Lys		Asp 725	Gly	His	Arg	Ile	Trp 730	Val	His					
	<210 <211 <212 <213	> 2 > D	4 066 0NA Iomo	sapi	ens												
	<220 <221 <222	. > C	DS (149)	(2	065)						·						
	<400 caca)> 1	.4 gcg c	ctcg	ctcg	ıc go	tcac	acac	gct	ctgc	ctc	ctct	ctcc	cg c	acgo	gcgca	60
																attga	120
	gctg	jaaga	aat t	tcca	ıgtga	ıc at	ttgt	aa a N	1et 1	acg c Thr F	cg c ro L	etc g Jeu A	sp S	cc a er A	gg c irg L	tc eu	172
Prof. flore three for first forth	caa Gln	gcg Ala 10	gcc Ala	cct Pro	gcc Ala	gcc Ala	gcc Ala 15	gcc Ala	gcc Ala	gcc Ala	Gly	ccg Pro 20	aag Lys	gtg Val	ccg Pro	ccg Pro	220
gi a	agc Ser 25	agt Ser	ctc Leu	cag Gln	cgc Arg	agg Arg 30	ctt Leu	cct Pro	tac Tyr	cgg Arg	gcg Ala 35	acc Thr	aca Thr	atg Met	tcc Ser	gag Glu 40	268
And the many than	ttt Phe	ctc Leu	ctc Leu	gcc Ala	tta Leu 45	ctc Leu	act Thr	ctc Leu	tcg Ser	gga Gly 50	tta Leu	ttg Leu	ccg Pro	att Ile	gcc Ala 55	agg Arg	316
	gtg Val	ctg Leu	acc Thr	gtg Val 60	gga Gly	gcc Ala	gac Asp	cga Arg	gat Asp 65	cag Gln	cag Gln	ttg Leu	tgt Cys	gat Asp 70	cct Pro	ggt Gly	364
	gaa Glu	ttt Phe	ctt Leu 75	tgc Cys	cac His	gat Asp	cac His	gtg Val 80	act Thr	tgt Cys	gtc Val	tcc Ser	cag Gln 85	agc Ser	tgg Trp	ctg Leu	412
	tgt Cys	gat Asp 90	gly ggg	gac Asp	cct Pro	Asp	tgc Cys 95	cct Pro	Asp	gat. Asp	Ser	Asp	Glu	tct Ser	tta Leu	gat Asp	460
	acc Thr 105	tgt Cys	ccc Pro	gag Glu	gag Glu	gta Val 110	gaa Glu	atc Ile	aag Lys	tgc Cys	Pro	ttg Leu	aat Asn	cac His	att Ile	gct Ala 120	508
	tgc Cys	ctt Leu	ggc Gly	acc Thr	aac Asn 125	aaa Lys	tgt Cys	gtt Val	cat His	tta Leu 130	tcc Ser	cag Gln	ctg Leu	tgc Cys	aat Asn 135	ggt Gly	556
	gtc Val	ttg Leu	gac Asp	tgc Cys 140	cca Pro	gat Asp	ggg Gly	tat Tyr	gac Asp 145	gaa Glu	gga Gly	gta Val	cat His	tgt Cys 150	cag Gln	gaa Glu	604
	ctg	tta	tcc	aat	tgc	caa	cag	ctg	aat	tgt	cag	tat	aaa	tgt	aca	atg	652

	Leu	Leu	Ser 155	Asn	Cys	Gln	Gln	Leu 160	Asn	Cys	Gln	Tyr	Lys 165	Cys	Thr	Met	
	gtc Val	aga Arg 170	aat Asn	agt Ser	aca Thr	aga Arg	tgt Cys 175	tac Tyr	tgt Cys	gag Glu	gat Asp	gga Gly 180	ttc Phe	gaa Glu	ata Ile	aca Thr	700
	gaa Glu 185	gat Asp	ggg Gly	aga Arg	agc Ser	tgt Cys 190	aaa Lys	gat Asp	caa Gln	gat Asp	gaa Glu 195	tgt Cys	gct Ala	gtt Val	tat Tyr	ggt Gly 200	748
	aca Thr	ggc Gly	agc Ser	cag Gln	acc Thr 205	tgc Cys	aga Arg	aac Asn	aca Thr	cat His 210	gga Gly	tcc Ser	tac Tyr	act Thr	tgc Cys 215	agt Ser	796
	tgt Cys	gtg Val	gaa Glu	ggc Gly 220	tac Tyr	cta Leu	atg Met	cag Gln	cca Pro 225	gac Asp	agc Ser	aga Arg	tct Ser	tgc Cys 230	aag Lys	gct Ala	844
	aaa Lys	att Ile	gaa Glu 235	cct Pro	aca Thr	gat Asp	aga Arg	cca Pro 240	cgt Arg	ata Ile	cta Leu	tta Leu	att Ile 245	gca Ala	aat Asn	ttt Phe	892
f 172 M.,	gaa Glu	tca Ser 250	att Ile	gag Glu	gtt Val	ttc Phe	tat Tyr 255	ctt Leu	aat Asn	gga Gly	agt Ser	aaa Lys 260	att Ile	gca Ala	act Thr	cta Leu	940
Hery Brit Bon harty Brit con	agc Ser 265	tca Ser	gtc Val	aat Asn	gga Gly	aat Asn 270	gaa Glu	att Ile	cat His	act. Thr	ctg Leu 275	gat Asp	ttt Phe	att Ile	tat Tyr	aat Asn 280	988
The state of the s	gaa Glu	gat Asp	gtg Val	att Ile	tgt Cys 285	tgg Trp	att Ile	gaa Glu	tca Ser	aga Arg 290	gaa Glu	tct; Ser	tca Ser	aat Asn	caa Gln 295	ctc Leu	1036
THE TOP IN	aaa Lys	tgt Cys	atc Ile	cag Gln 300	ata Ile	aca Thr	aaa Lys	gca Ala	gga Gly 305	gga Gly	tta Leu	aca Thr	gat Asp	gaa Glu 310	tgg Trp	aca Thr	1084
ing is	atc Ile	aat Asn	att Ile 315	ctt Leu	caa Gln	tcc Ser	ttc Phe	cac His 320	aat Asn	gtg Val	caa Gln	caa Gln	atg Met 325	gcg Ala	att Ile	gac Asp	1132
	tgg Trp	ctc Leu 330	Thr	cga Arg	aat Asn	ctc Leu	tat Tyr 335	ttt Phe	gtg Val	gac Asp	cat His	gtc Val 340	Gly	gac Asp	cgg Arg	atc Ile	1180
	ttt Phe 345	gtt Val	tgt Cys	aat Asn	tcc Ser	aac Asn 350	Gly	tct Ser	gta Val	tgt Cys	gto Val 355	Thr	ctg Leu	att Ile	gat Asp	ctg Leu 360	1228
	gag Glu	ctt Leu	cac His	aat Asn	cct Pro 365	aaa Lys	gca Ala	ata Ile	gca Ala	gta Val	Asp	cca Pro	ata Ile	gca Ala	gga Gly 375	aaa Lys	1276
	ctt Leu	ttc Phe	ttt Phe	act Thr 380	Asp	tac Tyr	ggg Gly	aat Asn	gtc Val 385	Ala	aaa Lys	ı gtg Val	gag Glu	aga Arg 390	Cys	gac Asp	1324
	atg Met	gat Asp	999 Gly 395	Met	aac Asn	cga Arg	aca Thr	agg Arg 400	Ile	att :Ile	gat Asp	tca Ser	aag Lys 405	Thr	gag Glu	g cag Gln	1372

	cca Pro	gct Ala 410	gca Ala	ctg Leu	gca Ala	cta Leu	gac Asp 415	cta Leu	gtc Val	aac Asn	aaa Lys	ttg Leu 420	gtt Val	tac Tyr	tgg Trp	gta Val	1420
	gat Asp 425	ctt Leu	tac Tyr	ttg Leu	gac Asp	tat Tyr 430	gtg Val	gga Gly	gta Val	gtg Val	gac Asp 435	tat Tyr	caa Gln	gga Gly	aaa Lys	aat Asn 440	1468
	aga Arg	cac His	act Thr	gtc Val	att Ile 445	caa Gln	ggc Gly	aga Arg	caa Gln	gtc Val 450	aga Arg	cat His	ctt Leu	tat Tyr	ggt Gly 455	ata Ile	1516
	act Thr	gtg Val	ttt Phe	gaa Glu 460	gat Asp	tat Tyr	ttg Leu	tat Tyr	gca Ala 465	acc Thr	aat Asn	tct Ser	gat Asp	aac Asn 470	tac Tyr	aat Asn	1564
	atc Ile	gta Val	agg Arg 475	ata Ile	aac Asn	cga Arg	ttt Phe	aat Asn 480	Gly ggg	act Thr	gat Asp	att Ile	cac His 485	tca. Ser	tta Leu	att Ile	1612
	aaa Lys	att Ile 490	gag Glu	aat Asn	gct Ala	tgg Trp	gga Gly 495	atc Ile	cga Arg	att Ile	tat Tyr	caa Gln 500	aaa Lys	aga Arg	act Thr	caa Gln	1660
Ann the part they	cca Pro 505	aca Thr	gtc Val	aga Arg	agc Ser	cat His 510	gca Ala	tgt Cys	gaa Glu	gtc Val	gat Asp 515	cca Pro	tat Tyr	gga Gly	atg Met	cca Pro 520	1708
Street fort forth	ggg Gly	ggc Gly	tgt Cys	tca Ser	cac His 525	atc Ile	tgt Cys	cta Leu	ctc Leu	agc Ser 530	agc Ser	agt Ser	tac Tyr	aaa Lys	act Thr 535	cgg Arg	1756
Transfer first the	act Thr	tgt Cys	cgc Arg	tgc Cys 540	agg Arg	act Thr	ggc Gly	ttc Phe	aac Asn 545	ttg Leu	gga Gly	agt Ser	gat Asp	ggc Gly 550	agg Arg	tca Ser	1804
	tgc Cys	aaa Lys	aga Arg 555	cca Pro	aag Lys	aat Asn	gag Glu	ttg Leu 560	ttc Phe	ctc Leu	ttt Phe	tat Tyr	999 Gly 565	aaa Lys	gga Gly	cgc Arg	1852
	cca Pro	gga Gly 570	att Ile	gtt Val	aga Arg	gga Gly	atg Met 575	gac Asp	ttg Leu	aat Asn	acc Thr	aag Lys 580	ata Ile	gct Ala	gat Asp	gaa Glu	1900
	tac Tyr 585	atg Met	atc Ile	ccc Pro	ata Ile	gaa Glu 590	aat Asn	ctg Leu	gta Val	aac Asn	cct Pro 595	cgt Arg	gct Ala	tta Leu	gac Asp	ttt Phe 600	1948
	cac His	gca Ala	gaa Glu	acc Thr	aat Asn 605	tac Tyr	atc Ile	tac Tyr	ttt Phe	gct Ala 610	Asp	acc Thr	acc Thr	agt Ser	ttc Phe 615	cta Leu	1996
	att Ile	ggc Gly	cgg Arg	cag Gln 620	Lys	ata Ile	gat Asp	ggc	aca Thr 625	gag Glu	aga Arg	gaa Glu	acc Thr	atc Ile 630	ctg Leu	aaa Lys	2044
	gat Asp	gat Asp	ctg Leu 635	Asp	aat Asn	gta Val	gag Glu	g									2066

<210> 15 <211> 639 <213> Homo sapiens

<400> 15

T M

7

Q1

Met Thr Pro Leu Asp Ser Arg Leu Gln Ala Ala Pro Ala Ala Ala Ala 1 5 10 15

Ala Ala Gly Pro Lys Val Pro Pro Ser Ser Leu Gln Arg Arg Leu Pro 20 25 30

Tyr Arg Ala Thr Thr Met Ser Glu Phe Leu Leu Ala Leu Leu Thr Leu 35 40 45

Ser Gly Leu Leu Pro Ile Ala Arg Val Leu Thr Val Gly Ala Asp Arg 50 55 60

Asp Gln Gln Leu Cys Asp Pro Gly Glu Phe Leu Cys His Asp His Val 65 70 75 80

Thr Cys Val Ser Gln Ser Trp Leu Cys Asp Gly Asp Pro Asp Cys Pro 85 90 95

Asp Asp Ser Asp Glu Ser Leu Asp Thr Cys Pro Glu Glu Val Glu Ile 100 105 110

. Lys Cys Pro Leu Asn His Ile Ala Cys Leu Gly Thr Asn Lys Cys Val 115 120 125

His Leu Ser Gln Leu Cys Asn Gly Val Leu Asp Cys Pro Asp Gly Tyr 130 135 140

Asp Glu Gly Val His Cys Gln Glu Leu Leu Ser Asn Cys Gln Gln Leu 145 150 155 160

Asn Cys Gln Tyr Lys Cys Thr Met Val Arg Asn Ser Thr Arg Cys Tyr $_{165}$ $_{170}$ $_{175}$

Cys Glu Asp Gly Phe Glu Ile Thr Glu Asp Gly Arg Ser Cys Lys Asp 180 185 190

Gln Asp Glu Cys Ala Val Tyr Gly Thr Gly Ser Gln Thr Cys Arg Asn 195 $$ 200 $$ 205

Thr His Gly Ser Tyr Thr Cys Ser Cys Val Glu Gly Tyr Leu Met Gln 210 215 220

Pro Asp Ser Arg Ser Cys Lys Ala Lys Ile Glu Pro Thr Asp Arg Pro 225 230 235 240

Arg Ile Leu Leu Ile Ala Asn Phe Glu Ser Ile Glu Val Phe Tyr Leu 245 250 255

Asn Gly Ser Lys Ile Ala Thr Leu Ser Ser Val Asn Gly Asn Glu Ile 260 265 270

His Thr Leu Asp Phe Ile Tyr Asn Glu Asp Val Ile Cys Trp Ile Glu 275 280 285

Ser Arg Glu Ser Ser Asn Gln Leu Lys Cys Ile Gln Ile Thr Lys Ala 290 295 300

Gly Gly Leu Thr Asp Glu Trp Thr Ile Asn Ile Leu Gln Ser Phe His 305 310 315 320

Asn Val Gln Gln Met Ala Ile Asp Trp Leu Thr Arg Asn Leu Tyr Phe 325 330 335

Val Asp His Val Gly Asp Arg Ile Phe Val Cys Asn Ser Asn Gly Ser 340 345 350

Val Cys Val Thr Leu Ile Asp Leu Glu Leu His Asn Pro Lys Ala Ile 355 360 365

Ala Val Asp Pro Ile Ala Gly Lys Leu Phe Phe Thr Asp Tyr Gly Asn 370 375 380

Val Ala Lys Val Glu Arg Cys Asp Met Asp Gly Met Asn Arg Thr Arg 385 390 390 395 400

Ile Ile Asp Ser Lys Thr Glu Gln Pro Ala Ala Leu Ala Leu Asp Leu 405 410 415

Val Asn Lys Leu Val Tyr Trp Val Asp Leu Tyr Leu Asp Tyr Val Gly
420 425 430

Val Val Asp Tyr Gln Gly Lys Asn Arg His Thr Val Ile Gln Gly Arg 435 440 445

Gln Val Arg His Leu Tyr Gly Ile Thr Val Phe Glu Asp Tyr Leu Tyr 450 455 460

Ala Thr Asn Ser Asp Asn Tyr Asn Ile Val Arg Ile Asn Arg Phe Asn 465 470 475 480

Gly Thr Asp Ile His Ser Leu Ile Lys Ile Glu Asn Ala Trp Gly Ile 485 490 495

Arg Ile Tyr Gln Lys Arg Thr Gln Pro Thr Val Arg Ser His Ala Cys 500 505 510	
Glu Val Asp Pro Tyr Gly Met Pro Gly Gly Cys Ser His Ile Cys Leu 515 520 525	
Leu Ser Ser Ser Tyr Lys Thr Arg Thr Cys Arg Cys Arg Thr Gly Phe 530 540	
Asn Leu Gly Ser Asp Gly Arg Ser Cys Lys Arg Pro Lys Asn Glu Leu 545 550 560	÷
Phe Leu Phe Tyr Gly Lys Gly Arg Pro Gly Ile Val Arg Gly Met Asp 565 570 575	
Leu Asn Thr Lys Ile Ala Asp Glu Tyr Met Ile Pro Ile Glu Asn Leu 580 585 590	
Val Asn Pro Arg Ala Leu Asp Phe His Ala Glu Thr Asn Tyr Ile Tyr 595 600 605	
Phe Ala Asp Thr Thr Ser Phe Leu Ile Gly Arg Gln Lys Ile Asp Gly 610 615 620	
Thr Glu Arg Glu Thr Ile Leu Lys Asp Asp Leu Asp Asn Val Glu 625 630 635	
<210> 16 <211> 1333 <212> DNA <213> Homo sapiens	
<220> <221> CDS <222> (280)(1323)	
<400> 16 gagatccaca cagctcggac cggctggatc ttgctcagtc tctgtcagag gaagatccct	60
tggaggaggc cccgcagcga catggaggga gctgctttgc tgaaagtctt tgtcctctgc	120
atotggaaco aaaatoactt cooggaattg accaactggt agactogoot agaggggaag	180
cattgtgtcc tagttgaggc taacagtcag tatccagcct caacattcag cagaggcccc	240
agatcagcgt ctgagccagg ccaacaatga ccaaggagg atg gga tcc tgg gtg Met Gly Ser Trp Val 1 5	294
cag ctc atc aca agc gtc ggg gtg cag caa aac cat cca ggc tgg aca Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn His Pro Gly Trp Thr 10 15 20	342

	gtg	gct	gga	cag	ttc	caa	gaa	aag	aaa	cgc	ttc	act	gaa	gaa	gtc	att	390
	Val	Ala	Gly	Gln 25	Phe	Gln	Glu	Lys	Tys	Arg	Phe	Thr	Glu	Glu 35	Val	Ile	
	gaa Glu	tac Tyr	ttc Phe 40	cag Gln	aag Lys	aaa Lys	gtt Val	agc Ser 45	cca Pro	gtg Val	cat His	ctg Leu	aaa Lys 50	atc Ile	ctg Leu	ctg Leu	438
	act Thr	agc Ser 55	gat Asp	gaa Glu	gcc Ala	tgg Trp	aag Lys 60	aga Arg	ttc Phe	gtg Val	cgt Arg	gtg Val 65	gct Ala	gaa Glu	ttg Leu	ccc Pro	486
	agg Arg 70	gaa Glu	gaa Glu	gca Ala	gat Asp	gct Ala 75	ctc Leu	tat Tyr	gaa Glu	gct Ala	ctg Leu 80	aag Lys	aat Asn	ctt Leu	aca Thr	cca Pro 85	534
	tat Tyr	gtg Val	gct Ala	att Ile	gag Glu 90	gac Asp	aaa Lys	gac Asp	atg Met	cag Gln 95	caa Gln	aaa Lys	gaa Glu	cag Gln	cag Gln 100	ttt Phe	582
F. T.	agg Arg	gag Glu	tgg Trp	ttt Phe 105	ttg Leu	aaa Lys	gag Glu	ttt Phe	cct Pro 110	caa Gln	atc Ile	aga Arg	tgg Trp	aag Lys 115	att Ile	cag Gln	630
To The The	gag Glu	tcc Ser	ata Ile 120	gaa Glu	agg Arg	ctt Leu	cgt Arg	gtc Val 125	att Ile	gca Ala	aat Asn	gag Glu	att Ile 130	gaa Glu	aag Lys	gtc Val	678
The Property of the second	cac His	aga Arg 135	ggc Gly	tgc Cys	gtc Val	atc Ile	gcc Ala 140	aat Asn	gtg Val	gtg Val	tct Ser	ggc Gly 145	tcc Ser	act Thr	ggc Gly	atc Ile	726
	ctg Leu 150	tct Ser	gtc Val	att Ile	ggc Gly	gtt Val 155	atg Met	ttg Leu	gca Ala	cca Pro	ttt Phe 160	aca Thr	gca Ala	gly aaa	ct.g Leu	agc Ser 165	774
	ctg Leu	agc Ser	att Ile	act Thr	gca Ala 170	gct Ala	gly ggg	gta Val	gly ggg	ctg Leu 175	gga Gly	ata Ile	gca Ala	tct Ser	gcc Ala 180	acg Thr	822
	gct Ala	gly ggg	atc Ile	gcc Ala 185	tcc Ser	agc Ser	atc Ile	gtg Val	gag Glu 190	aac Asn	aca Thr	tac Tyr	aca Thr	agg Arg 195	tca Ser	gca Ala	870
,	gaa Glu	ctc Leu	aca Thr 200	gcc Ala	agc Ser	agg Arg	ctg Leu	act Thr 205	gca Ala	acc Thr	agc Ser	act Thr	gac Asp 210	caa Gln	ttg Leu	gag Glu	918
	gca Ala	tta Leu 215	Arg	gac Asp	att Ile	ctg Leu	cgt Arg 220	gac Asp	atc Ile	aca Thr	ccc Pro	aat Asn 225	Val	ctt Leu	tct Ser	ttt Phe	966.
	gca Ala 230	Leu	gat Asp	ttt Phe	gac Asp	gaa Glu 235	gcc Ala	aca Thr	aaa Lys	atg Met	att Ile 240	Ala	aat Asn	gat Asp	gtc Val	cat His 245	1014
	aca Thr	ctc Leu	agg Arg	aga Arg	tct Ser 250	aaa Lys	gcc Ala	act Thr	gtt Val	gga Gly 255	Arg	cct Pro	ttg Leu	att Ile	gct Ala 260	tgg Trp	1062
	cga Arg	tat Tyr	gta Val	cct Pro 265	Ile	aat Asn	gtt Val	gtt Val	gag Glu 270	Thr	ctg Leu	aga Arg	aca Thr	cgt Arg 275	Gly	gcc Ala	1110

									-								
ccc Pro	acc Thr	cgg Arg 280	ata Ile	gtg Val	aga Arg	aaa Lys	gta Val 285	gcc Ala	cgg Arg	aac Asn	ctg Leu	ggc Gly 290	aag Lys	gcc Ala	act Thr	1.1	58
tca Ser	ggt Gly 295	gtc Val	ctt Leu	gtt Val	gtg Val	ctg Leu 300	gat Asp	gta Val	gtc Val	aac Asn	ctt Leu 305	gtg Val	caa Gln	gac Asp	tca Ser	12	206
ctg Leu 310	gac Asp	ttg Leu	cac His	aag Lys	ggg Gly 315	gca Ala	aaa Lys	tcc Ser	gag Glu	tct Ser 320	gct Ala	gag Glu	tcg Ser	ctg Leu	agg Arg 325	12	254
cag Gln	tgg Trp	gct Ala	cag Gln	gag Glu 330	ctg Leu	gag Glu	gag Glu	aat Asn	ctc Leu 335	aat Asn	gag Glu	ctc Leu	acc Thr	cat His 340	atc Ile	13	302
	_	agt Ser			_		tagg	gecea	aat				,		·	13	333
<21 <21 <21 <21	1> : 2> :	17 348 PRT Homo	·sap:	iens													
<40	0 >	17															
Met 1	Gly	Ser	Trp	Val 5	Gln	Leu	Ile	Thr	Ser 10	Val	Gly	Val	Gln	Gln 15	Asn		
His	Pro	Gly	Trp 20	Thr	Val	Ala	Gly	Gln. 25	Phe	Gln	Glu	Lys	Tys	Arg	Phe		
Thr	Glu	Glu 35	Val	Ile	Glu	Tyr	Phe 40	Gln	Lys	Lys	Val	Ser 45	Pro	Val	His		
Leu	Lys 50	Ile	Leu	Leu	Thr	Ser 55	Asp	Glu	Ala	Trp	Lys 60	Arg	Phe	Val	Arg		•
Val 65	Ala	Glu	Leu	Pro	Arg 70	Glu	Glu	Ala	Asp	Ala 75	Leu	Tyr	Glu	Ala	Leu 80		
Lys	Asn	Leu	Thr	Pro 85	Тун	Val	Ala	Ile	Glu 90	Asp	Lys	Asp	Met	Gl.n 95	Gln		
Lys	Glu	Gln	Gln 100	Phe	Arg	Glu	Trp	Phe 105	Leu	Lys	Glu	Phe	Pro 110	Gln	Ile		
Arg	Trp	Lys 115		Gln	Glu	Ser	Ile 120		Arg	Leu	Arg	Val 125		Ala	Asn		
Glu	Ile 130		Lys	Val	His	Arg 135		Cys	Val	Ile	Ala 140		Val	Val	Ser		

Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe 145 150 155 160

Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly 165 170 175

Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr 180 185 190

Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser 195 200 205

Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu Arg Asp Ile Thr Pro 210 215 220

Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile 225 230 235 240

Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg 245 250 255

Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu 260 265 270

Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn 275 280 285

Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn 290 295 300

Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser 305 310 315 320

Ala Glu Ser Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn 325 330 335

Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly 340

<210> 18

<211> 1490

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (151)..(1170)

<400> 18

agcaaaagag aaaaggagcc aggctgggct tcctgatccc acagcatcgc agagctcggg

aggo	acag	ct c	acag	acac	a gg	aaac	acag	gad	tgct	att	ctgc	tctc	ct g	ссса	cggtg	120
atct	ggtg	cc a	gctg	ıgtgg	ja ac	agtg	ggtg	atg Met 1	gcg Ala	tcc Ser	ctg Leu	ctg Leu 5	caa Gln	gac Asp	cag Gln	174
ctg Leu	acc Thr 10	act Thr	gat Asp	cag Gln	gac Asp	ttg Leu 15	ctg Leu	ctg Leu	atg Met	cag Gln	gaa Glu 20	ggc Gly	atg Met	ccg Pro	atg Met	222
cgc Arg 25:	aag Lys	gtg Val	agg Arg	tcc Ser	aaa Lys 30	agc Ser	tgg Trp	aag Lys	aag Lys ,	cta Leu 35	aga Arg	tac Tyr	ttc Phe	aga Arg	ctt Leu 40	270
cag Gln	aat Asn	gac Asp	ggc Gly	atg Met 45	aca Thr	gtc Val	tgg Trp	cat His	gca Ala 50	cgg Arg	cag Gln	gcc Ala	agg Arg	ggc Gly 55	agt Ser	318
gcc Ala	aag Lys	ccc Pro	agc Ser 60	ttc Phe	tca Ser	atc Ile	tct Ser	gat Asp 65	gtg Val	gag Glu	aca Thr	ata Ile	cgt Arg 70	aat Asn	ggc Gly	366
cat His	gat Asp	tcc Ser 75	gag Glu	ttg Leu	ctg Leu	cgt Arg	agc Ser 80	ctg Leu	gca Ala	gag Glu	gag Glu	ctc Leu 85	ccc Pro	ctg Leu	gag Glu	414
cag Gln	ggc Gly 90	ttc Phe	acc Thr	att Ile	gtc Val	ttc Phe 95	cat His	ggc Gly	cgc Arg	cgc Arg	tcc Ser 100	aac Asn	ctg Leu	gac Asp	ctg Leu	462
atg Met 105	gcc Ala	aac Asn	agt Ser	gtt Val	gag Glu 110	gag Glu	gcc Ala	cag Gln	Ile	tgg Trp 115	atg Met	cga Arg	Gly 999	ctc Leu	cag Gln 120	510
ctg Leu	ttg Leu	gtg Val	gat Asp	ctt Leu 125	gtc Val	acc Thr	agc Ser	atg Met	gac Asp 130	cat His	cag Gln	gag Glu	cgc Arg	ctg Leu 135	gac Asp	558
caa Gln	tgg Trp	ctg Leu	agc Ser 140	gat Asp	tgg Trp	ttt Phe	caa Gln	cgt Arg 145	gga Gly	gac Asp	aaa Lys	aat Asn	cag Gln 150	gat Asp	ggt Gly	606
aag Lys	atg Met	agt Ser 155	ttc Phe	caa Gln	gaa Glu	gtt Val	cag Gln 160	cgg Arg	tta Leu	ttg Leu	cac His	cta Leu 165	atg Met	aat Asn	gtg Val	654
gaa Glu	atg Met 170	gac Asp	caa Gln	gaa Glu	tat Tyr	gcc Ala 175	ttc Phe	agt Ser	ctt Leu	ttt Phe	cag Gln 180	gca Ala	gca Ala	gac Asp	acg Thr	702
tcc Ser 185	cag Gln	tct Ser	gga Gly	acc Thr	ctg Leu 190	gaa Glu	gga Gly	gaa Glu	gaa Glu	ttc Phe 195	gta Val	cag Gln	ttc Phe	tat Tyr	aag Lys 200	750
gca Ala	ttg Leu	act Thr	aaa Lys	cgt Arg 205	gct Ala	gag Glu	gtg Val	cag Gln	gaa Glu 210	ctg Leu	ttt Phe	gaa Glu	agt Ser	ttt Phe 215	tca Ser	798
gct Ala	gat Asp	ggg Gly	cag Gln 220	aag Lys	ctg Leu	act Thr	ctg Leu	ctg Leu 225	gaa Glu	ttt Phe	ttg Leu	gat Asp	ttc Phe 230	ctc Leu	caa Gln	846
gag	gag	cag	aag	gag	aga	gac	tgc	acc	tct	gag	ctt	gct	ctg	gaa	ctc	894

Glu	Glu	Gln 235	Lys	Glu	Arg	Asp	Cys 240	Thr	Ser	Glu	Leu	Ala 245	Leu	Glu	Leu	
att Ile	gac Asp 250	cgc Arg	tat Tyr	gaa Glu	cct Pro	tca Ser 255	gac Asp	agt Ser	ggc Gly	aaa Lys	ctg Leu 260	cgg Arg	cat His	gtg Val	ctg Leu	942
agt Ser 265	atg Met	gat Asp	ggc Gly	ttc Phe	ctc Leu 270	agc Ser	tac Tyr	ctc Leu	tgc Cys	tct Ser 275	aag Lys	gat Asp	gga Gly	gac Asp	atc Ile 280	990
tto Phe	aac Asn	cca Pro	gcc Ala	tgc Cys 285	ctc Leu	ccc Pro	atc Ile	tat Tyr	cag Gln 290	gat Asp	atg Met	act Thr	caa Gln	ccc Pro 295	ctg Leu	1038
aac Ası	c cac n His	tac Tyr	ttc Phe 300	atc Ile	tgc Cys	tct Ser	tct Ser	cat His 305	aac Asn	acc Thr	tac Tyr	cta Leu	gtg Val 310	ggg Gly	gac Asp	1086
caç Gl:	g ctt n Leu	tgc Cys 315	Gly	cag Gln	agc Ser	agc Ser	gtc Val 320	gag Glu	gga Gly	tat Tyr	ata Ile	cgg Arg 325	tgc Cys	agt Ser	ggt Gly	1134
gg Gl	aga Arg 330	Glu	gly ggg	gtc Val	caa Gln	ctc Leu 335	atg Met	aga Arg	Gly 999	acc Thr	atg Met 340	tag	aaaa	gtg		1180
ag	gggag	ctg	tcag	tgtc	ta a	caga	ttgg	g ac	agtg	ttgt	ggg	ggtt	tag	äddc	tgagga	1240
gc	cctgg	ata	ccag	agac	ac t	tgga	ggag	a ta	ttga	agac	tgg	tggg	aga	atgg	taatga	1300
aa	cccta	tgg	gtca	atgg	aa c	ttct	cttt	c ac	aagc	tatg	aaa	ctct	cct	ggaa	ctcaga	1360
99	ccctg	aca	gatt	tata	tt t	aaca	aatt	a at	aaac	agat	tgt	taaa	tgg	aagg	caatag	1420
ag	aatag	gag	ttaa	aaat	at a	ggtt	ctgg	a gt	caga	ccat	ctg	aaat	tat	attc	tagctc	1480
ct	ttact	tgg														1490
	10> 11>	19 340														

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Ser Leu Leu Gln Asp Gln Leu Thr Thr Asp Gln Asp Leu Leu 10

Leu Met Gln Glu Gly Met Pro Met Arg Lys Val Arg Ser Lys Ser Trp

Lys Lys Leu Arg Tyr Phe Arg Leu Gln Asn Asp Gly Met Thr Val Trp

His Ala Arg Gln Ala Arg Gly Ser Ala Lys Pro Ser Phe Ser Ile Ser 55 50

Asp Val Glu Thr Ile Arg Asn Gly His Asp Ser Glu Leu Leu Arg Ser 65 70 75 80

Leu Ala Glu Glu Leu Pro Leu Glu Gln Gly Phe Thr Ile Val Phe His 85 90 95

Gly Arg Arg Ser Asn Leu Asp Leu Met Ala Asn Ser Val Glu Glu Ala 100 105 110

Gln Ile Trp Met Arg Gly Leu Gln Leu Leu Val Asp Leu Val Thr Ser 115 120 125

Met Asp His Gln Glu Arg Leu Asp Gln Trp Leu Ser Asp Trp Phe Gln 130 135 140

Arg Gly Asp Lys Asn Gln Asp Gly Lys Met Ser Phe Gln Glu Val Gln 145 150 155 160

Arg Leu Leu His Leu Met Asn Val Glu Met Asp Gln Glu Tyr Ala Phe 165 170 175

Ser Leu Phe Gln Ala Ala Asp Thr Ser Gln Ser Gly Thr Leu Glu Gly 180 185 190

Glu Glu Phe Val Gln Phe Tyr Lys Ala Leu Thr Lys Arg Ala Glu Val 195 200 205

Gln Glu Leu Phe Glu Ser Phe Ser Ala Asp Gly Gln Lys Leu Thr Leu 210 215 220

Leu Glu Phe Leu Asp Phe Leu Gln Glu Gln Lys Glu Arg Asp Cys 225 230 230 235

Thr Ser Glu Leu Ala Leu Glu Leu Ile Asp Arg Tyr Glu Pro Ser Asp 245 250 255

Ser Gly Lys Leu Arg His Val Leu Ser Met Asp Gly Phe Leu Ser Tyr 260 265 270

Leu Cys Ser Lys Asp Gly Asp Ile Phe Asn Pro Ala Cys Leu Pro Ile 275 280 285

Tyr Gln Asp Met Thr Gln Pro Leu Asn His Tyr Phe Ile Cys Ser Ser 290 295 300

His Asn Thr Tyr Leu Val Gly Asp Gln Leu Cys Gly Gln Ser Ser Val 305 310 315 320

Glu Gly Tyr Ile Arg Cys Ser Gly Gly Arg Glu Gly Val Gln Leu Met 325 335

Arg Gly Thr Met 340

<210> 20 <211> 2035 <212> DNA <213> Homo sapiens	
<220> <221> CDS <222> (189)(1415)	
<400> 20 ccaactaagc ttgcctaatt tgcttcagaa ttggaagagg gaattgcagc aggaaaatat	60
gtgaagagtt tttaaaccca caaattcttc ttactttaga attagttgtt acattggcag	120
gaaaaaataa atgcagatgt tggaccatgt tggaaacctt gtcaagacag tggattgtct	180
cacacaga atg gaa atg tgg ctt ctg att ctg gtg gcg tat atg ttc cag Met Glu Met Trp Leu Leu Ile Leu Val Ala Tyr Met Phe Gln 1 5 10	230
aga aat gtg aat tca gta cat atg cca act aaa gct gtg gac cca gaa Arg Asn Val Asn Ser Val His Met Pro Thr Lys Ala Val Asp Pro Glu 15 20 25 30	278
gca ttc atg aat att agt gaa atc atc caa cat caa ggc tat ccc tgt Ala Phe Met Asn Ile Ser Glu Ile Ile Gln His Gln Gly Tyr Pro Cys 35 40 45	326
gag gaa tat gaa gtc gca act gaa gat ggg tat atc ctt tct gtt aac Glu Glu Tyr Glu Val Ala Thr Glu Asp Gly Tyr Ile Leu Ser Val Asn 50 55 60	374
agg att cct cga ggc cta gtg caa cct aag aag aca ggt tcc agg cct Arg Ile Pro Arg Gly Leu Val Gln Pro Lys Lys Thr Gly Ser Arg Pro 65 70 75	422
gtg gtg tta ctg cag cat ggc cta gtt gga ggt gct agc aac tgg att Val Val Leu Leu Gln His Gly Leu Val Gly Gly Ala Ser Asn Trp Ile 80 85 90	470
too aac ctg ccc aac aat agc ctg ggc ttc att ctg gca gat gct ggt Ser Asn Leu Pro Asn Asn Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly 95 100 105 110	518
ttt gac gtg tgg atg ggg aac agc agg gga aac gcc tgg tct cga aaa Phe Asp Val Trp Met Gly Asn Ser Arg Gly Asn Ala Trp Ser Arg Lys 115 120 125	566
cac aag aca ctc tcc ata gac caa gat gag ttc tgg gct ttc agt tat His Lys Thr Leu Ser Ile Asp Gln Asp Glu Phe Trp Ala Phe Ser Tyr 130 135 140	614
gat gag atg gct agg ttt gac ctt cct gca gtg ata aac ttt att ttg Asp Glu Met Ala Arg Phe Asp Leu Pro Ala Val Ile Asn Phe Ile Leu 145 150 155	662

L. W.	Jirl.
	'hill
	Tare.
Į,	1100
Harry Company	HISTORY
Į.	4
Ch Jin	4,445
===	į
44	;
=	
=	
=	
The first state offer	H. S. R. Mark
The first state offer	H. S. R. Mark
The first state offer	H. S. R. Mark
in ffing Buffe	Think and HT 42 Phigh

cag Gln	aaa Lys 160	acg Thr	ggc Gly	cag Gln	gaa Glu	aag Lys 165	atc Ile	tat Tyr	tat Tyr	gtc Val	ggc Gly 170	tat Tyr	tca Ser	cag Gln	ggc Gly	710
acc Thr 175	acc Thr	atg Met	ggc Gly	ttt Phe	att Ile 180	gca Ala	ttt Phe	tcc Ser	acc Thr	atg Met 185	cca Pro	gag Glu	ctg Leu	gct Ala	cag Gln 190	758
aaa Lys	atc Ile	aaa Lys	atg Met	tat Tyr 195	ttt Phe	gct Ala	tta Leu	gca Ala	ccc Pro 200	ata Ile	gcc Ala	act Thr	gtt Val	aag Lys 205	cat His	806
gca Ala	aaa Lys	agc Ser	ccc Pro 210	ggg Gly	acc Thr	aaa Lys	ttt Phe	ttg Leu 215	ttg Leu	ctg Leu	cca Pro	gat Asp	atg Met 220	atg Met	atc Ile	854
aag Lys	gga Gly :	Leu	ttt Phe	ggc Gly	aaa Lys	aaa Lys	gaa Glu 230	ttt Phe	ctg Leu	tat Tyr	cag Gln	acc Thr 235	aga Arg	ttt Phe	ctc Leu	902
aga Arg	caa Gln 240	ctt Leu	gtt Val	att Ile	tac Tyr	ctt Leu 245	tgt Cys	ggc Gly	cag Gln	gtg Val	att Ile 250	ctt Leu	gat Asp	cag Gln	att Ile	950
tgt Cys 255	agt Ser	aat Asn	atc Ile	atg Met	tta Leu 260	ctt Leu	ctg Leu	ggt Gly	gga Gly	ttc Phe 265	aac Asn	acc Thr	aac Asn	aat Asn	atg Met 270	998
aac Asn	atg Met	agc Ser	cga Arg	gca Ala 275	agt Ser	gta Val	tat Tyr	gct Ala	gcc Ala 280	cac His	act Thr	ctt Leu	gct. Ala	gga Gly 285	aca Thr	1046
tct Ser	gtg Val	caa Gln	aat Asn 290	att Ile	cta Leu	cac His	tgg Trp	agc Ser 295	cag Gln	gca Ala	gtg Val	aat Asn	tct Ser 300	ggt Gly	gaa Glu	1094
ctc Leu	cgg Arg	gca Ala 305	ttt Phe	gac Asp	tgg Trp	gly aaa	agt Ser 310	gag Glu	acc Thr	aaa Lys	aat Asn	ctg Leu 315	gaa Glu	aaa Lys	tgc Cys	1142.
aat Asn	cag Gln 320	cca Pro	act Thr	cct Pro	gta Val	agg Arg 325	tac Tyr	aga Arg	gtc Val	aga Arg	gat Asp 330	atg Met	acg Thr	gtc Val	cct Pro	1190
aca Thr 335	gca Ala	atg Met	tgg Trp	aca Thr	gga Gly 340	ggt Gly	cag Gln	gac Asp	tgg Trp	ctt Leu 345	Ser	aat Asn	cca Pro	gaa Glu	gac Asp 350	1238
gtg Val	aaa Lys	atg Met	ctg Leu	ctc Leu 355	tct Ser	gag Glu	gtg Val	acc Thr	aac Asn 360	ctc Leu	atc Ile	tac Tyr	cat His	aag Lys 365	Asn	1286
att Ile	cct Pro	gaa Glu	tgg Trp 370	Ala	cat His	gtg Val	gat Asp	ttc Phe 375	atc Ile	tgg Trp	ggt Gly	ttg Leu	gat Asp 380	Ala	cct Pro	1334
cac His	cgt Arg	atg Met 385	Tyr	aat Asn	gaa Glu	atc Ile	atc Ile 390	cat His	ctg Leų	atg Met	cag Gln	cag Gln 395	Glu	gag Glu	acc Thr	1382
		Ser				tgt Cys 405						agca	tct	gaca	ctgacg	1435

atcttaggac	aacctcctga	gggatggggc	taggacccat	gaaggcagaa	ttatggagag	1495
cagagaccta	gtatacattt	ttcagattcc	ctgcacttgg	cactaaatcc	gacacttaca	1555
tttacatttt	ttttctgtaa	attaaagtac	ttattaggta	aatagaggtt	ttgtatgcta	1615
ttatatattc	taccatcttg	aagggtaggt	tttacctgat	agccagaaaa	tatctagaca	1675
ttctctatat	cattcaggta	aatctcttta	aaacacctat	tgttttttct	ataagccata	1735
tttttggagc	actaaagtaa	aatggcaaat	tgggacagat	attgaggtct	ggagtctgtg	1795
gattattgtt	gactttgaca	aaataagcta	gacattttca	ccttgttgcc	acagagacat	1855
aacactacct	caggaagctg	agctgcttta	aggacaacaa	caacaaaatc	agtgttacag	1915
tatggatgaa	atctatgtta	agcattctca	gaataaggcc	aagttttata	gttgcatctc	1975
agggaagaaa	attttatagg	atgtttatga	gttctccaat	aaatgcattc	tgcattacat	2035

<210> 21 <211> 409 <212> PRT

<213> Homo sapiens

<400> 21

Met Glu Met Trp Leu Leu Ile Leu Val Ala Tyr Met Phe Gln Arg Asn 1 5 10 15

Val Asn Ser Val His Met Pro Thr Lys Ala Val Asp Pro Glu Ala Phe 20 25 30

Met Asn Ile Ser Glu Ile Ile Gln His Gln Gly Tyr Pro Cys Glu Glu 35 40 45

Tyr Glu Val Ala Thr Glu Asp Gly Tyr Ile Leu Ser Val Asn Arg Ile 50 55 60

Pro Arg Gly Leu Val Gln Pro Lys Lys Thr Gly Ser Arg Pro Val Val 65 70 75 80

Leu Leu Gln His Gly Leu Val Gly Gly Ala Ser Asn Trp Ile Ser Asn 85 90 95

Leu Pro Asn Asn Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly Phe Asp 100 105 110

Val Trp Met Gly Asn Ser Arg Gly Asn Ala Trp Ser Arg Lys His Lys
115 120 125

Thr Leu Ser Ile Asp Gln Asp Glu Phe Trp Ala Phe Ser Tyr Asp Glu 130 135 140 Met Ala Arg Phe Asp Leu Pro Ala Val Ile Asn Phe Ile Leu Gln Lys 145 150 155 160

Thr Gly Gln Glu Lys Ile Tyr Tyr Val Gly Tyr Ser Gln Gly Thr Thr 165 170 175

Met Gly Phe Ile Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Lys Ile 180 185 190

Lys Met Tyr Phe Ala Leu Ala Pro Ile Ala Thr Val Lys His Ala Lys 195 200 205

Ser Pro Gly Thr Lys Phe Leu Leu Pro Asp Met Met Ile Lys Gly 210 215 220

Leu Phe Gly Lys Lys Glu Phe Leu Tyr Gln Thr Arg Phe Leu Arg Gln 225 230 235 240

Leu Val Ile Tyr Leu Cys Gly Gln Val Ile Leu Asp Gln Ile Cys Ser 245 250 255

Asn Ile Met Leu Leu Gly Gly Phe Asn Thr Asn Asn Met Asn Met 260 265 270

Ser Arg Ala Ser Val Tyr Ala Ala His Thr Leu Ala Gly Thr Ser Val 275 280 285

Gln Asn Ile Leu His Trp Ser Gln Ala Val Asn Ser Gly Glu Leu Arg 290 295 300

Ala Phe Asp Trp Gly Ser Glu Thr Lys Asn Leu Glu Lys Cys Asn Gln 305 310 315 320

Pro Thr Pro Val Arg Tyr Arg Val Arg Asp Met Thr Val Pro Thr Ala 325 330 335

Met Trp Thr Gly Gly Gln Asp Trp Leu Ser Asn Pro Glu Asp Val Lys 340 345 350

Met Leu Leu Ser Glu Val Thr Asn Leu Ile Tyr His Lys Asn Ile Pro 355 360 365

Glu Trp Ala His Val Asp Phe Ile Trp Gly Leu Asp Ala Pro His Arg 370 375 380

Met Tyr Asn Glu Ile Ile His Leu Met Gln Gln Glu Glu Thr Asn Leu 385 390 395 400

Ser Gln Gly Arg Cys Glu Ala Val Leu 405

<210><211><212><212><213>	22 2224 DNA Homo	sapi	ens												
<220> <221> <223>	misc_ n = a	_		go	r t										
<220> <221> CDS <222> (82)(921) <223> Xaa = Unknown or other															
<400> tgcttc	22 ctga a	actaç	jctca	ıc ag	ıtago	ccgg	g egg	gecea	aggg	caat	ccga	icc a	acatt	tcact	60
ctcacc	gctg t	agga	atco	a g	atg Met 1	cag Gln	gcc Ala	aag Lys	tac Tyr 5	agc Ser	agc Ser	acg Thr	agg Arg	gac Asp 10	111
atg ct Met Le	g gat u Asp	gat Asp	gat Asp 15	G].Y 999	gac Asp	acc Thr	acc Thr	atg Met 20	agc Ser	ctg Leu	cat His	tct Ser	caa Gln 25	gcc Ala	159
tct go Ser Al	c aca a Thr	act Thr 30	cgg Arg	cat His	cca Pro	gag Glu	ccc Pro 35	cgg Arg	cgc Arg	aca Thr	gag Glu	cac His 40	agg Arg	gct Ala	207
ccc to Pro Se	t tca er Ser 45	acg Thr	tgg Trp	cga Arg	cca Pro	gtg Val 50	gcc Ala	ctg Leu	acc Thr	ctg Leu	ctg Leu 55	act Thr	ttg Leu	tgc Cys	255
ttg gt Leu Va	ıl Leu	ctg Leu	ata Ile	ggg Gly	ctg Leu 65	gca Ala	gcc Ala	ctg Leu	gly aaa	ctt Leu 70	ttg Leu	ttt Phe	ttt Phe	cag Gln	303
tac ta Tyr Ty 75	ıc cag vr Gln	ctc Leu	tcc Ser	aat Asn 80	act Thr	ggt Gly	caa Gln	gac Asp	acc Thr 85	att Ile	tct Ser	caa Gln	atg Met	gaa Glu 90	351
gaa ag Glu Ar	ga tta cg Leu	gga Gly	aat Asn 95	acg Thr	tcc Ser	caa Gln	gag Glu	ttg Leu 100	caa Gln	tct Ser	ctt Leu	caa Gln	gtc Val 105	cag Gln	399
aat at Asn Il	a aag le Lys	ctt Leu 110	gca Ala	gga Gly	agt Ser	ctg Leu	cag Gln 115	cat His	gtg Val	gct Ala	gaa Glu	aaa Lys 120	ctc Leu	tgt Cys	447
cgt ga Arg Gl	ag ctg lu Leu 125	Tyr	aac Asn	aaa Lys	gct Ala	gga Gly 130	gca Ala	cac His	agg Arg	tgc Cys	agc Ser 135	cct Pro	t.gt Cys	aca Thr	495
gaa ca Glu Gl 14	aa tgg ln Trp 40	aaa Lys	tgg Trp	cat His	gga Gly 145	gac Asp	aat Asn	tgc Cys	tac Tyr	cag Gln 150	ttc Phe	tat Tyr	aaa Lys	gac Asp	543

agc Ser 155	aaa Lys	agt Ser	tgg Trp	gag Glu	gac Asp 160	tgt Cys	aaa Lys	tat Tyr	ttc Phe	tgc Cys 165	ctt Leu	agt Ser	gaa Glu	aac Asn	tct Ser 170	591
acc Thr	atg Met	ctg Leu	aag Lys	ata Ile 175	aac Asn	aaa Lys	caa Gln	gaa Glu	gac Asp 180	ctg Leu	gaa Glu	ttt Phe	gcc Ala	gcg Ala 185	tct Ser	639
cag Gln	agc Ser	tac Tyr	tct Ser 190	gag Glu	ttt Phe	ttc Phe	tac Tyr	tct Ser 195	tat Tyr	tgg Trp	aca Thr	gly gag	ctt Leu 200	ttg Leu	cgc Arg	687
cct Pro	gac Asp	agt Ser 205	ggc Gly	aag Lys	gcc Ala	tgg Trp	ctg Leu 210	tgg Trp	atg Met	gat Asp	gga Gly	acc Thr 215	cct Pro	ttc Phe	act Thr	735
tct Ser	gaa Glu 220	ctg Leu	ttc Phe	cat His	att Ile	ata Ile 225	ata Ile	gat Asp	gtc Val	acc Thr	agc Ser 230	cca Pro	aga Arg	agc Ser	aga Arg	783
gac Asp 235	tgt Cys	gtg Val	gcc Ala	atc Ile	ctt Leu 240	aat Asn	ggg Gly	atg Met	atc Ile	ttc Phe 245	tca Ser	aag Lys	gac Asp	tgc Cys	aaa Lys 250	831
gaa Glu	ttg Leu	aag Lys	cgt Arg	tgt Cys 255	gtc Val	tgt Cys	gag Glu	aga Arg	agg Arg 260	gca Ala	gga Gly	atg Met	gtg Val	aag Lys 265	cca Pro	879
gag Glu	agc Ser	ctc Leu	cat His 270	Val	ccc Pro	cct Pro	gaa Glu	aca Thr 275	tta Leu	ggc Gly	gaa Glu	ggt Gly	gac Asp 280			921
tga	ttcg	ccc	tctg	caac	ta c	aaat	agca	g ag	tgag	ccag	gcg	gtgc	caa	agca	agggct	981
agt	tgag	aca	ttgg	gaaa	tg g	aaca	taat	c ag	gaaa	gact	atc	tata	tga	ctag	tacaaa	1041
atg	ggtt	ctc	gtgt	ttcc	tg t	tcag	gatc	а сс	agca	tttc	tga	gctt	9 99	ttta	tgcacg	1101
tat	ttaa	cag	tcac	aaga	ag t	ctta	ttta	c at	gcca	ccaa	cca	acct	cag	aaac	ccataa	1161
tgt	catc	tgc	cttc	ttgg	ct t	agag	ataa	c tt	ttag	ctċt	ctt	tctt	ctc	aatg	tctaat	1221
atc	acct	ccc	tgtt	ttca	tg t	cttc	ctta	c ac	ttgg	tgga	ata	agaa	act	tttt	gaagta	1281
gag	gaaa	tac	attg	aggt	aa c	atcc	tttt	c tc	tgac	agtc	aag	tagt	сса	tcag	aaattg	1341
gca	gtca	ctt	ccca	gatt	gt a	ccag	caaa	t ac	acaa	ggaa	ttc	tttt '	tgt	ttgt	ttcagt	1401
															ccgttt	1461
															attcct	1521
															aggaaa	1581
															tcagag	1641
															gttcct	1701
															aataaa	1761
															aattca	1821
gca	tgga	aat	gctt	ttca	aa a	tatg	atag	ic aa	tcat	tatt	ttg	attg	tgc	ctta	ıctgaaa	1881

gtttttgggg aatttacaag agtactgatt acatgattat ctggagaaaa taagatgtct 1941
ttgaaataca tgttggcttc aagaaaacag ttttaacgtt ttcctaaaat gaaatctttt 2001
gaggtgagct tatggcatca acacatggtt gatgaggaag ctgagttgca ttagtgcaca 2061
tgatttccag tcaggtcatg ggaaatgaac agagacagtg acatctttgt agctgctcct 2121
ttgtgaggca cttctttctt gagatgactc catgcacaaa tataacaggg atcattggga 2181
atgacaccat cacagccacc aagnttattg ggttactgat aat 2224

<210> 23

<211> 280

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> n = \overline{a} or c or g or t

<400> 23

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Gly $_1$ 5 10 15

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His 20 25 30

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg 35 40 45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly 50 55 60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn 65 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr 85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly 100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys 115 120 125

Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His 130 135 140

Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp 145 150 155

Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn 165 170 175	
Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe 180 185 190	
Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala 195 200 205	
Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile 210 215 220	
Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu 225 230 235 240	
Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val 245 250 255	
Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro 260 265 270	•
Pro Glu Thr Leu Gly Glu Gly Asp 275 280	
<210> 24 <211> 996 <212> DNA <213> Homo sapiens	
<211> 996 <212> DNA	
<211> 996 <212> DNA <213> Homo sapiens <220> <221> CDS	gc 55 er
<pre><211> 996 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (38)(979) <400> 24 ccgaccacat ttcactctca ccgctgtggg aatccag atg cag gcc aag tac ag Met Gln Ala Lys Tyr Se</pre>	er g 103
<pre><211> 996 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (38)(979) <400> 24 ccgaccacat ttcactctca ccgctgtggg aatccag atg cag gcc aag tac ag</pre>	er g 103 ı
<pre> <211> 996 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (38)(979) <400> 24 ccgaccacat ttcactctca ccgctgtggg aatccag atg cag gcc aag tac ag</pre>	g 103 u 151 r 199
<pre> <211> 996 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (38)(979) <400> 24 ccgaccacat ttcactctca ccgctgtggg aatccag atg cag gcc aag tac ag</pre>	103 1 103 1 151 1 199 1 199

Leu	Phe	Phe	Gln	Tyr 75	Tyr	Gln	Leu	Ser	Asn 80	Thr	Gly	Gln	Asp	Thr 85	Ile	
tct Ser	caa Gln	atg Met	gaa Glu 90	gaa Glu	aga Arg	tta Leu	gga Gly	aat Asn 95	acg Thr	tcc Ser	caa Gln	gag Glu	ttg Leu 100	caa Gln	tct Ser	343
ctt Leu	caa Gln	gtc Val 105	cag Gln	aat Asn	ata Ile	aag Lys	ctt Leu 110	gca Ala	gga Gly	agt Ser	ctg Leu	cag Gln 115	cat His	gtg Val	gct Ala	391
gaa Glu	aaa Lys 120	ctc Leu	tgt Cys	cgt Arg	gag Glu	ctg Leu 125	tat Tyr	aac Asn	aaa Lys	gct Ala	gga Gly 130	ggc Gly	tat Tyr.	aca Thr	aga Arg	439
aac Asn 135	atg Met	gtg Val	cca Pro	gca Ala	tct Ser 140	gct Ala	tct Ser	tct Ser	gag Glu	agc Ser 145	ctc Leu	agg Arg	cag Gln	ctt Leu	cca Pro 150	487
cac His	atg Met	ggg Gly	gaa Glu	agt Ser 155	gca Ala	gca Ala	gca Ala	cac His	agg Arg 160	tgc Cys	agc Ser	cct Pro	tgt Cys	aca Thr 165	gaa Glu	535
caa Gln	tgg Trp	aaa Lys	tgg Trp 170	cat His	gga Gly	gac Asp	aat Asn	tgc Cys 175	tac Tyr	cag Gln	ttc Phe	tat Tyr	aaa Lys 180	gac Asp	agc Ser	583
aaa Lys	agt Ser	tgg Trp 185	gag Glu	gac Asp	tgt Cys	aaa Lys	tat Tyr 190	ttc Phe	tgc Cys	ctt Leu	agt Ser	gaa Glu 195	aac Asn	tct Ser	acc Thr	631.
atg Met	ctg Leu 200	aag Lys	ata Ile	aac Asn	aaa Lys	caa Gln 205	gaa Glu	gac Asp	ctg Leu	gaa Glu	ttt Phe 210	gcc Ala	gcg Ala	tct Ser	cag Gln	679
agc Ser 215	tac Tyr	tct Ser	gag Glu	ttt Phe	ttc Phe 220	tac Tyr	tct Ser	tat Tyr	tgg Trp	aca Thr 225	61y 999	ctt Leu	ttg Leu	ogc Arg	cct Pro 230	727
gac Asp	agt Ser	ggc Gly	aag Lys	gcc Ala 235	tgg Trp	ctg Leu	tgg Trp	atg Met	gat Asp 240	gga Gly	acc Thr	cct Pro	ttc Phe	act Thr 245	tct Ser	775 _:
gaa Glu	ctg Leu	ttc Phe	cat His 250	att Ile	ata Ile	ata Ile	gat Asp	gtc Val 255	acc Thr	agc Ser	cca Pro	aga Arg	agc Ser 260	aga Arg	gac Asp	823
tgt Cys	gtg Val	gcc Ala 265	atc Ile	ctt Leu	aat Asn	ggg Gly	atg Met 270	atc Ile	ttc Phe	tca Ser	aag Lys	gac Asp 275	tgc Cys	aaa Lys	gaa Glu	871
ttg Leu	aag Lys 280	cgt Arg	tgt Cys	gtc Val	tgt Cys	gag Glu 285	aga Arg	agg Arg	gca Ala	gga Gly	atg Met 290	gtg Val	aag Lys	cca Pro	gag Glu	919
agc Ser 295	ctc Leu	cat His	gtc Val	ccc Pro	cct Pro 300	gaa Glu	aca Thr	tta Leu	ggc Gly	gaa Glu 305	Gly	gac Asp	atg Met	cat His	cat His 310	967
	cat His			_	ccta	ggt	tcta	gac								996

<210> 25

<211> 314

<212> PRT

<213> Homo sapiens

<400> 25

Met Gln Ala Lys Tyr Ser Ser Thr Met Asp Met Leu Asp Asp Gly
1 5 10 15

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His 20 25 30

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg 35 40 45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly 50 55 60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn 65 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr 85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys 115 120 125

Ala Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu 130 135 140

Ser Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala His Arg 145 150 155 1.60

Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr 165 170 175

Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys 180 185 190

Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu 195 200 205

Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp 210 215 220

Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp 225 230 235 240	
Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr 245 250 255	
Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe 260 265 270	
Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala 275 280 285	
Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly 290 295 300	
Glu Gly Asp Met His His His His His 305 310	
<210> 26 <211> 2125 <212> DNA <213> Homo sapiens	
<220> <221> misc_feature	
<223> n = a cr c or g or t	
<pre><220> <221> CDS <222> (82)(822) <223> Xaa = Unknown or other</pre>	
<220> <221> CDS <222> (82)(822) <223> Xaa = Unknown or other <400> 26	60
<220> <221> CDS <222> (82)(822) <223> Xaa = Unknown or other	60 111
<pre><220> <221> CDS <222> (82)(822) <223> Xaa = Unknown or other <400> 26 tgcttcctga actagctcac agtagcccgg cggcccaggg caatccgacc acatttcact ctcaccgctg taggaatcca g atg cag gcc aag tac agc agc acg agg gac</pre>	
<pre> <220> <221> CDS <222> (82)(822) <223> Xaa = Unknown or other <400> 26 tgcttcctga actagctcac agtagcccgg cggcccaggg caatccgacc acatttcact ctcaccgctg taggaatcca g atg cag gcc aag tac agc agc acg agg gac</pre>	111
<pre><220> <221> CDS <222> (82)(822) <223> Xaa = Unknown or other </pre> <pre> <400> 26 tgcttcctga actagctcac agtagcccgg cggcccaggg caatccgacc acatttcact ctcaccgctg taggaatcca g atg cag gcc aag tac agc acg agg gac</pre>	111

ata aag ctt gca gga agt ctg cag cat gtg gct gaa aaa ctc tgt cgt Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg 75 80 85 90	351
gag ctg tat aac aaa gct gga gca cac agg tgc agc cct tgt aca gaa Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu 95 100 105	399
caa tgg aaa tgg cat gga gac aat tgc tac cag ttc tat aaa gac agc Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser 110 115 120	447
aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa aac tct acc Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr 125 130 135	495
atg ctg aag ata aac aaa caa gaa gac ctg gaa ttt gcc gcg tct cag Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln 140 145 150	543
age tac tot gag tit the tac tot tat tgg aca ggg of tit ttg ogc oct Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro 155 160 165 170	591
gac agt ggc aag gcc tgg ctg tgg atg gat gga acc cct ttc act tct Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser 175 180 185	639
gaa ctg ttc cat att ata ata gat gtc acc agc cca aga agc aga gac Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp 190 195 200	687
tgt gtg gcc atc ctt aat ggg atg atc ttc tca aag gac tgc aaa gaa Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu 205 210 215	735
ttg aag cgt tgt gtc tgt gag aga agg gca gga atg gtg aag cca gag Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu 220 225 230	783
age etc cat gtc ecc ect gaa aca tta gge gaa ggt gae tgattegeee Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp 235 240 245	832.
tctgcaacta caaatagcag agtgagccag gcggtgccaa agcaagggct agttgagaca	892
ttgggaaatg gaacataatc aggaaagact atctctctga ctagtacaaa atgggttctc	952
gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgcacg tatttaacag	1012
tcacaagaag tettatttae atgecaceaa ecaaceteag aaaceeataa tgteatetge	1072
cttcttggct tagagataac ttttagctct ctttcttctc aatgtctaat atcacctccc	1132
tgttttcatg tcttccttac acttggtgga ataagaaact ttttgaagta gaggaaatac	1192
attgaggtaa catcetttte tetgacagte aagtagteea teagaaattg geagteaett	1252
cccagattgt accagcaaat acacaaggaa ttetttttgt ttgtttcagt tcatactagt	1312
cccttcccaa tccatcagta aagaccccat ctgccttgtc catgccgttt cccaacaggg	1372
atgtcacttg atatgagaat ctcaaatctc aatgccttat aagcattcct tcctgtgtcc	1432

<210>

27

```
attaagactc tgataattgt ctcccctcca taggaatttc tcccaggaaa gaaatatatc
                                                                     1492
cccatctccg tttcatatca gaactaccgt ccccqatatt cccttcagaq aqattaaaqa
                                                                     1552
ccagaaaaaa gtgagcctct tcatctgcac ctgtaatagt ttcagttcct attttcttcc
                                                                     1612
attgacccat atttatacct ttcaggtact gaagatttaa taataataaa tgtaaatact
                                                                     1672
gtgaagtgtg tgtgatttta caatggactt atggttggtg ggaaaattca gcatggaaat
                                                                     1732
getttteaaa atatgatage ggteattatt tigattgtge ettaetgaaa gtitttgggg
                                                                     1792
aatttacaag agtactgatt acatgattat ctggagaaaa taagatgtct ttgaaataca
                                                                     1852
tgttggcttc aagaaaacag ttttaacgtt ttcctaaaat gaaatctttt gaggtgagct
                                                                     1912
tatggcatca acacatggtt gatgaggaag ctgagttgca ttagtgcaca tgatttccaq
                                                                     1972
traggtratg ggaaatgaar agagaragtg aratetttqt agetqeteet ttqtqaqqea
                                                                     2032
cttctttctt gagatgactc catgcacaaa tataacaggg atcattggga atgacaccat
                                                                     2092
cacagocaco aagnttattg ggttactgat aat
                                                                     2125
```

```
<211> 247
<212> PRT
<213> Homo sapiens
<220>
<221> misc_feature
<223> n = a or c or g or t
<400> 27
```

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Gly 1 10 15

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His 20 25 30

Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser Asn Thr 35 40 45

Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser 50 55 60

Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser 65 70 75 80

Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala 85 90 95

Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly 100 105 110

Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys 115 120 125	
Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys 130 135 140	
Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe 145 150 155 160	
Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp 165 170 175	
Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile 180 185 190	
Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn 195 200 205	
Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys 210 215 220	
Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro 225 240	
Glu Thr Leu Gly Glu Gly Asp 245	
<210> 28 <211> 5059 <212> DNA <213> Homo sapiens	
<220> <221> CDS <222> (199)(2457)	
<400> 28 cgggaggaat ggaaggagaa ggcggaatgt gggagggctc agggggatgt gggagggacg	60
aacggagaag ggggagagag gggggtccag tctcccctgg ccgagcattt ttttttttgg	120
aagteetagg aetgatetee aggaceagea etetteteee ageeettagg gteetgeteg	180
gccaaggcet teeetgee atg ega eet gte agt gte tgg eag tgg age eee Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro 1 5 10	231
tgg ggg ctg ctg tgc ctg ctg tgc agt tcg tgc ttg ggg tct ccg Trp Gly Leu Leu Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro 15 20 25	279
tcc cct tcc acg ggc cct gag aag aag gcc ggg agc cag ggg ctt cgg Ser Pro Ser Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg 30 35 40	327

	ttc Phe	cgg Arg 45	ctg Leu	gct Ala	ggc Gly	ttc Phe	ccc Pro 50	agg Arg	aag Lys	ccc Pro	tac Tyr	gag Glu 55	ggc Gly	cgc Arg	gtg Val	gag Glu	375
	ata Ile 60	cag Gln	cga Arg	gct Ala	ggt Gly	gaa Glu 65	tgg Trp	ggc Gly	acc Thr	atc Ile	tgc Cys 70	gat Asp	gat Asp	gac Asp	ttc Phe	acg Thr 75	423
	ctg Leu	cag Gln	gct Ala	gcc Ala	cac His 80	atc Ile	ctc Leu	tgc Cys	cgg Arg	gag Glu 85	ctg Leu	ggc Gly	ttc Phe	aca Thr	gag Glu 90	gcc Ala	471
,	aca Thr	ggc Gly	tgg Trp	acc Thr 95	cac His	agt Ser	gcc Ala	aaa Lys	tat Tyr 100	ggc Gly	cct Pro	gga. Gly	aca Thr	ggc Gly 105	cgc Arg	atc Ile	519
	tgg Trp	ctg Leu	gac Asp 110	aac Asn	ttg Leu	agc Ser	tgc Cys	agt Ser 115	999 Gly	acc Thr	gag Glu	cag. Gln	agt Ser 120	gtg Val	act Thr	gaa Glu	567
A CONG. JOHN.	tgt Cys	gcc Ala 125	tcc Ser	cgg Arg	ggc Gly	tgg Trp	999 Gly 130	aac Asn	agt Ser	gac Asp	tgt Cys	acg Thr 135	cac His	gat Asp	gag Glu	gat Asp	615
	gct Ala 140	Gly 999	gtc Val	atc Ile	tgc Cys	aaa Lys 145	gac Asp	cag Gln	cgc Arg	ctc Leu	cct Pro 150	ggc Gly	ttc Phe	tcg Ser	gac Asp	tcc Ser 155	663
The first two that a	aat Asn	gtc Val	att Ile	gag Glu	gta Val 160	gag Glu	cat His	cac His	ctg Leu	caa Gln 165	gtg Val	gag Glu	gag Glu	gtg Val	cga Arg 170	att Ile	711
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	cga Arg	ccc Pro	gcc Ala	gtt Val 175	999 Gly	tgg Trp	ggc Gly	aga Arg	cga Arg 180	ccc Pro	ctg Leu	ccc Pro	gtg Val	acg Thr 185	gag Glu	Gly 999	75 [.] 9
A THE THE	ctg Leu	gtg Val	gaa Glu 190	gtc Val	agg Arg	ctt Leu	cct Pro	gac Asp 195	ggc	tgg Trp	tcg Ser	caa Gln	gtg Val 200	tgc Cys	gac Asp	aaa Lys	807
	ggc Gly	t.gg Trp 205	agc Ser	gcc Ala	cac His	aac Asn	agc Ser 210	cac His	gtg Val	gtc Val	tgc Cys	999 Gly 215	atg Met	ctg Leu	ggc Gly	ttc Phe	855
	ccc Pro 220	agc Ser	gaa Glu	aag Lys	agg Arg	gtc Val 225	aac Asn	gcg Ala	gcc Ala	Phe	tac Tyr 230	agg Arg	ctg Leu	cta Leu	gcc Ala	caa Gln 235	903
	cgg Arg	cạg Gln	caa Gln	cac His	tcc Ser 240	ttt Phe	ggt Gly	ctg Leu	cat His	999 Gly 245	gtg Val	gcg Ala	tgc Cys	gtg Val	ggc Gly 250	\mathtt{Thr}	951
	gag Glu	gcc Ala	cac His	ctc Leu 255	tcc Ser	ctc Leu	tgt Cys	tcc Ser	ctg Leu 260	gag Glu	ttc Phe	tat Tyr	cgt Arg	gcc Ala 265	aat Asn	gac Asp	999
	acc Thr	gcc Ala	agg Arg 270	tgc Cys	cct Pro	ggg Gly	ggg ggg	ggc Gly 275	cct Pro	gca Ala	gtg Val	gtg Val	agc Ser 230	tgt Cys	gtg Val	cca Pro	1047
	ggc Gly	cct Pro 285	gtc Val	tac Tyr	gcg Ala	gca Ala	tcc Ser 290	agt Ser	ggc Gly	cag Gln	aag Lys	aag Lys 295	Gln	caa Gln	cag Gln	tcg Ser	1095

aag cct cag ggg gag gtc cgt gtc cgt cta aag ggc ggc gcc cac cct

Lys Pro Gln Gly Glu Val Arg Val Arg Leu Lys Gly Gly Ala His Pro

this still The street with the still still

gcg gaa gag aac tgc ctg gcc agc tca gcc cgc tca gcc aac tgg ccc Ala Glu Glu Asn Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro 560 565 570	1911
tat ggt cac cgg cgt ctg ctc cga ttc tcc tcc cag atc cac aac ctg Tyr Gly His Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu 575 580 585	1959
gga cga gct gac ttc agg ccc aag gct ggg cgc cac tcc tgg gtg tgg Gly Arg Ala Asp Phe Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp 590 595 600	2007
cac gag tgc cat ggg cat tac cac agc atg gac ttc ttc act cac tat His Glu Cys His Gly His Tyr His Ser Met Asp Phe Phe Thr His Tyr 605 610 615	2055
gat atc ctc acc cca aat ggc acc aag gtg gct gag ggc cac aaa gct Asp Ile Leu Thr Pro Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala 620 625 630 635	
agt ttc tgt ctc gaa gac act gag tgt cag gag gat gtc tcc aag cgg Ser Phe Cys Leu Glu Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg 640 645 650	2151
tat gag tgt gcc aac ttt gga gag caa ggc atc act gtg ggt tgc tgg Tyr Glu Cvs Ala Asn Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp 655 660 665	2199
gat ctc tac cgg cat gac att gac tgt cag tgg att gac atc acg gat Asp Leu Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp 670 680	2247
gtg aag cca gga aac tac att ctc cag gtt gtc atc aac cca aac ttt Val Lys Pro Gly Asn Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe 685 690 695	2295
gaa gta gca gag agt gac ttt acc aac aat gca atg aaa tgt aac tgc Glu Val Ala Glu Ser Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys 700 705 710 715	•
aaa tat gat gga cat aga atc tgg gtg cac aac tgc cac att ggt gat Lys Tyr Asp Gly His Arg Ile Trp Val His Asn Cys His Ile Gly Asp 720 725 730	2391
gcc ttc agt gaa gag gcc aac agg agg ttt gaa cgc tac cct ggc cac Ala Phe Ser Glu Glu Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Glr 735 740 745	g 2439 n
acc agc aac cag att atc taagtgccac tgccctctgc aaaccaccac Thr Ser Asn Gln Ile Ile 750	2487
tggcccctaa tggcaggggt ctgaggctgc cattacctca ggagcttacc aagaaacc	cca 2547
tgtcagcaac cgcactcatc agaccatgca ctatggatgt ggaactgtca agcagaag	gtt 2607
ttcaccctcc ttcagaggcc agctgtcagt atctgtagcc aagcatggga atctttg	etc 2667
ccaggcccag caccgagcag aacagaccag agcccaccac accacaaaga gcagcacc	ctg 2727
actaactgcc cacaaaagat ggcagcagct cattttcttt aataggaggt caggatg	gtc 2787
agetecagta teteceetaa gtttaggggg atacagettt acetetagee ttttggtg	ggg 2847

,	ggaaaagatc	cagccctccc	acctcatttt	ttactataat	atgttgctag	gtataatttt	2907
	attttatata	aaaagtgttt	ctgtgattct	tcagagccca	ggagtcagtg	ctggtggttg	2967
	gagggacctg	ccccactgg	ttcatttaac	cctctgtctc	ggtgccctca	gaacctcagc	3027
	cagaaaggca	aggaggaaat	cagagcagga	gcctcatact	cttggtgatc	tattcattct	3087
	gtgacctcag	gggtcacata	taaggtcagt	gtttctcgtc	cccgccggat	ctgcactgcc	3147
	aactgggatt	gggttcgaac	agcttcataa	acatcttcag	cattttgtac	catctgctcc	3207
	ccaatggcca	aaatcacatc	accaggccgc	agaccagccc	ggtgtgcagg	ggagcccagg	3267
	atgactttat	ggatgagtac	accatgctga	acatcgggaa	agcttggttc	tcgaagctgt	3327
	agttcagcaa	ggatgctggg	actcagggtc	agcatcatca	ccccaatgta	gcgccgctgg	3387
	gacccactga	ttccggagga	ggaattcttc	ttttccccac	gatgcagaaa	ctctcgaaga	3447
	cgatcagaag	ggatggcaaa	ggagattcca	gctgtgacct	tcatggtgtt	cactccaatc	3507
	acctccccat	ccaggttaac	caggggacct	ccagagtttc	caaaatcaat	agctgcatca	3567
	gtttgaatgt	attocacatt	ggtttggggg	agtcccaggt	ctctggctgg	acgctgagca	3627
	gagctaacaa	tgccggatgt	gatcgtgttc	tgcagtgcaa	agggacttcc	catggcaaca	3687
	acaaactccc	.cttgccggac	atcagctgag	cgtcccagag	gcagcgtggg	gagaggetee	3747.
	ttagtctgaa	tcctcagcgt	tgcgatgtct	gccacgggat	ccacagctgt	gaccacggcc	3807
	tcatacgtgt	cgccgcttag	cagtctcaca	cggactctgc	gccgatcagc	caccacatgg	3867
	gcgttggtga	caatgagccc	atcggcagcc	accacgaatc	ctgagccgtt	cgagataggg	3927
	acctcgcggc	ccaagaaagg	gtgccggtcc	aggatctcga	tatagaccac	ggcaggtgct	3987
	gtcttctcca	ccacatctgc	gatgaagttg	tactgactcc	ggggagaagc	gggcggcggg	4047
	ctagggacgg	cggcgaggac	ggccggagga	ccccgacccc	cgccccacaa	caacaacagc	4107
	actgccccc	cagegeecag	cgccaccgcc	agccacgcgc	gcgaacgggt	tccagagttc	4167
	tctgaggcct	cccgggtcct	ggtatctggg	gtcaccgcag	tcagttgtgc	ccggggaccc	4227
	ggggtcccag	acgtcaggca	tgctcggggt	tcagtgaccc	caacagacaa	ccgggcccag	4287
	agactggggg	tcccataagt	cactcgggcc	cgggggtcag	aagttcctga	cgtcagcagg	4347
	gcccggaggt	caggggtcaa	acggggtctc	ctccccagc	gaatgccccc	caaagcccgc	4407
	catgcccgaa	ggctccagcc	tgcaccccgc	cccgccctcg	gcgcagccat	cagctccgcc	4467
	ttggctgcct	cctcgcccgc	cctactcaga	ggcggcaccc	aggacgcgag	caggcggaca	4527
	gtaggacgcg	gggcacgccg	gtacctgaag	tccttcagaa	gtgcacgccg	ggaccaggat	4587
	tccgggaggc	cgactcctcc	ctgccccacg	aatgccggga	attgtggtct	ccgccggacg	4547
	cgagttgtga	gacggcccaa	ggggccgcgg	ggtatgctgg	gaccgctagc	cattaaggag	4707
	cgcctcagga	cttcgggtcc	cctcaccccg	ggcggatgcc	caaagactcc	gccttcccaa	4767

gagcccctgc	ggccgggcgc	gaaaatggcg	gcggcggcga	cggccgggcg	ctcctgaagc	4827
agcagttatg	gagcttccct	cagggccggg	gccggagcgg	ctctttgact	cgcaccggta	4887
agagacccgg	cgggaagaga	ccgatccccg	cgtgctctcg	gccttcggcg	cctgaccact	4947
tcgcctctcg	cccccaggct	tccgggtgac	tgettectac	tgctcgtgct	gctgctctac	5007
gcgccagtcg	ggttctgcct	cctcgtcctg	cgcctctttc	tcgggatcca	cg	5059

<210> 29 <211> 753 <212> PRT

<213> Homo sapiens

<400> 29

Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu 10

Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly 20

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly 50

Glu Trp Gly Thr Ile Cys Asp Asp Phe Thr Leu Gln Ala Ala His 70

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His 90 85

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu 105

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly 120

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys 135

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val 150

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly 170 165

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His

195 Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg 215 210 Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser 230 Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro 265 Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu Val Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Tyr Arg Lys Trp 335 Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser . 345 340 Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala 355 Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp 370 375 Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln 385 Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg

Ile Arg Leu Ser Gly Gly Arg Ser Glo His Glu Gly Arg Val Glu Val 425

420

41 Ľ) Q1 **=** C1 ļ. Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp 435 440 445

Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu 450 455 460

Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly 470 475 480

Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu 485 490 495

Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys 500 505 510

Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala 515 520 525

Ser Asp Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile 530 535 540

Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys 545 550 555 560

Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg 565 570 575

Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe 580 585 590

Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly 595 600 605

His Tyr His Ser Met Asp Phe Phe Thr His Tyr Asp Ile Leu Thr Pro 610 615 620

Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu 625 630 635 640

Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn 645 650 655

Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His

Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn 675 680 685

Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser

695

Asp Phe Thr	Asn Asn Ala 710	Met Lys Cys	Asn Cys Lys 715	s Tyr Asp Gly	His 720
Arg Ile Trp	Val His Asn 725	Cys His Ile	Gly Asp Ala	a: Phe Ser Glu 735	Glu
Ala Asn Arg	Arg Phe Glu 740	Arg Tyr Pro 745	Gly Gln Th	r Ser Asn Gln 750	Ile
Ile			:		
<210> 30 <211> 4552 <212> DNA <213> Homo	s sapiens				
<220> <221> CDS <222> (127	7)(1950)				
		•		tttttggaa gt.cct	
taatctccag	gaccagcact c	ttctcccag cc	cttagggt cc	etgetegge caage	gaatta 120
cctgcc atg Met :- 1	cga cct gtc Arg Pro Val	agt gtc tgg Ser Val Trp 5	cag tgg agc Gln Trp Ser 10	c ccc tgg ggg (r Pro Trp Gly)	etg 168 Leu
Met 1 cta cta ta	Arg Pro Val	Ser Val Trp 5 agt tcg tgc	Gln Trp Ser 10 ttg ggg tc	c ccc tgg ggg c r Pro Trp Gly l ct cca tcc cct er Pro Ser Pro	Leu tcc 216
Met 1 ctg ctg tgg Leu Leu Cy 15:	Arg Pro Val c ctg ctg tgc s Leu Leu Cys 20	Ser Val Trp 5 agt tcg tgc Ser Ser Cys	Gln Trp Ser 10 ttg ggg tc Leu Gly Se 25 cag ggg ct	r Pro Trp Gly ct cca tcc cct	tcc 216 Ser 30 ctg 264
Met 1 ctg ctg tgg Leu Leu Cys 15: acg ggc cc Thr Gly Pro	Arg Pro Val c ctg ctg tgc s Leu Leu Cys 20 t gag aag aag c Glu Lys Lys 35	Ser Val Trp 5 agt tcg tgc Ser Ser Cys g gcc ggg agc Ala Gly Ser	Cln Trp Ser 10 ttg ggg tc Leu Gly Se 25 cag ggg ct Gln Gly Le 40 ggc cgc gt Gly Arg Va	et coa too oot er Pro Ser Pro et cgg tto cgg eu Arg Phe Arg	tcc 216 Ser 30 ctg 264 Leu cga 312
ctg ctg tgc Leu Leu Cy: 15: acg ggc cc Thr Gly Pro	Arg Pro Val c ctg ctg tgc s Leu Leu Cys 20 t gag aag aag c Glu Lys Lys 35 c ccc agg aag e Pro Arg Lys 50 a tqq qqc acc	Ser Val Trp 5 agt tcg tgc Ser Ser Cys g gcc ggg agc Ala Gly Ser g ccc tac gag Pro Tyr Glu 55 atc tgc gat	ttg ggg tc Leu Gly Se 25 cag ggg ct Gln Gly Le 40 ggc cgc gt Gly Arg Va	et cca tcc cct er Pro Ser Pro et cgg ttc cgg eu Arg Phe Arg 45 tg gag ata cag al Glu Ile Gln	tcc 216 Ser 30 ctg 264 Leu cga 312 Arg
ctg ctg tgc Leu Leu Cys 15: acg ggc ccc Thr Gly Pro gct ggc ttc Ala Gly Ph gct ggt ga Ala Gly Gl 65 gcc cac at	Arg Pro Val c ctg ctg tgc s Leu Leu Cys 20 t gag aag aag o Glu Lys Lys 35 c ccc agg aag e Pro Arg Lys 50 a tgg ggc acc u Trp Gly Thi	Ser Val Trp 5 agt tcg tgc Ser Ser Cys g gcc ggg agc Ala Gly Ser g ccc tac gag Pro Tyr Glu 55 atc tgc gat Tle Cys Asp 70 g qag ctg ggc	Cln Trp Ser 10 ttg ggg tc Leu Gly Se 25 cag ggg ct Gln Gly Le 40 ggc cgc gt Gly Arg Va gat gac tt Asp Asp Ph	ct cca tcc cct er Pro Ser Pro et cgg ttc cgg eu Arg Phe Arg 45 et gag ata cag al Glu Ile Gln 60 et acg ctg cag he Thr Leu Gln 75 ag gcc aca ggc lu Ala Thr Gly	tcc 216 Ser 30 ctg 264 Leu cga 312 Arg gct 360 Ala tgg 408
ctg ctg tgg Leu Leu Cy: 15: acg ggc cc: Thr Gly Pro gct ggc tt Ala Gly Ph gct ggt ga Ala Gly Gl 65 gcc cac at Ala His Il 80 acc cac ag	Arg Pro Val c ctg ctg tgc s Leu Leu Cys 20 t gag aag aag o Glu Lys Lys 35 c ccc agg aag e Pro Arg Lys 50 a tgg ggc acc u Trp Gly Thi c ctc tgc cgg e Leu Cys Arg	Ser Val Trp 5 agt tcg tgc Ser Ser Cys g gcc ggg agc Ala Gly Ser g ccc tac gag Pro Tyr Glu 55 atc tgc gat Tle Cys Asp 70 g gag ctg ggc g Glu Leu Gly 85 aggc cct gga r Gly Pro Gly	ttg ggg tc Leu Gly Se 25 cag ggg ct Gln Gly Le 40 ggc cgc gt Gly Arg Va gat gac tt Asp Asp Ph ttc aca ga Phe Thr Gl	ct cca tcc cct er Pro Ser Pro et cgg ttc cgg eu Arg Phe Arg 45 et gag ata cag al Glu Ile Gln 60 et acg ctg cag he Thr Leu Gln 75 ag gcc aca ggc lu Ala Thr Gly	tcc 216 Ser 30 ctg 264 Leu cga 312 Arg gct 360 Ala tgg 408 Trp gac 456

Asn	Leu	Ser	Cys	Ser 115	Gly	Thr	Glu	Gln	Ser 120	Val	Thr	Glu	Cys	Ala 125	Ser	
cgg Arg	ggc Gly	tgg Trp	999 Gly 130	aac Asn	agt Ser	gac Asp	tgt Cys	acg Thr 135	cac His	gat Asp	gag Glu	gat Asp	gct Ala 140	ggg Gly	gtc Val	552
atc Ile	tgc Cys	aaa Lys 145	gac Asp	cag Gln	cgc Arg	ctc Leu	cct Pro 150	ggc Gly	ttc Phe	tcg Ser	gac Asp	tcc Ser 155	aat Asn	gtc Val	att Ile	600
gag Glu	gcc Ala 160	cgt Arg	gtc Val	cgt Arg	cta Leu	aag Lys 165	ggc Gly	ggc Gly	gcc Ala	cac His	cct Pro 170	gga Gly	gag Glu	ggc Gly	cgg Arg	648
gta Val 175	gaa Glu	gtc Val	ct.g Leu	aag Lys	gcc Ala 180	agc Ser	aca Thr	tgg Trp	ggc Gly	aca Thr 185	gtc Val	tgt Cys	gac Asp	egc Arg	aag Lys 190	696
tgg Trp	gac Asp	ctg Leu	cat His	gca Ala 195	gcc Ala	agc Ser	gtg Val	gtg Val	tgt Cys 200	cgg Arg	gag Glu	ctg Leu	ggc Gly	ttc Phe 205	ggg Gly	744
agt Ser	gct Ala	cga Arg	gaa Glu 210	gct Ala	ctg Leu	agt Ser	ggc Gly	gct Ala 215	cgc Arg	atg Met	ggg Gly	cag Gln	ggc Gly 220	atg Met	ggt Gly	792
gct Ala	atc Ile	cac His 225	ctg Leu	agt Ser	gaa Glu	gtt Val	cgc Arg 230	tgc Cys	tct Ser	gga Gly	cag Gln	gag Glu 235	ctc Leu	tcc Ser	ctc Leu	840
tgg Trp	aag Lys 240	tgc Cys	ccc Pro	cac His	aag Lys	aac Asn 245	atc Ile	aca Thr	gct Ala	gag Glu	gat Asp 250	tgt Cys	tca Ser	cat His	agc Ser	888
cag Gln 255	gat. Asp	gcc Ala	gly 999	gtc Val	cgg Arg 260	tgc Cys	aac Asn	ct.a Leu	cct Pro	tac Tyr 265	act	gjà aaa	gca Ala	gag Glu	acc Thr 270	936
agg Arg	atc Ile	cga Arg	ctc Leu	agt Ser 275	Gly 999	ggc Gly	cgc Arg	agc Ser	caa Gln 280	cat His	gag Glu	ggg Gly	cga Arg	gtc Val 285	gag Glu	984
gtg Val	caa Gln	ata Ile	999 Gly 290	gga Gly	cct Pro	61 A aaa	ccc Pro	ctt Leu 295	cgc Arg	tgg Trp	ggc	ctc Leu	atc Ile 300	tgt Cys	G17.	1032
gat Asp	gac Asp	tgg Trp 305	Gly 999	acc Thr	ctg Leu	gag Glu	gcc Ala 310	atg Met	gtg Val	gcc Ala	tgt Cys	agg Arg 315	caa Gln	ctg Leu	ggt Gly	1080
ctg Leu	ggc Gly 320	Tyr	gcc Ala	aac Asn	cac His	ggc Gly 325	ctg Leu	cag Gln	gag Glu	acc Thr	tgg Trp 330	tac Tyr	tgg Trp	gac Asp	tct Ser	1128
999 Gly 335	Asn	ata Ile	aca Thr	gag Glu	gtg Val 340	gtg Val	atg Met	agt Ser	gga Gly	gtg Val 345	Arg	tgc Cys	aca Thr	gly aaa	act Thr 350	1176
gag Glu	ctg Leu	tcc Ser	ctg Leu	gat Asp 355	cag Gln	tgt Cys	gcc Ala	cat His	cat His 360	ggc Gly	acc Thr	cac His	atc Ile	acc Thr 365	Cys	1224

	aag Lys	agg Arg	aca Thr	999 Gly 370	acc Thr	cgc Arg	ttc Phe	act Thr	gct Ala 375	gga Gly	gtc Val	atc Ile	tgt Cys	tct Ser 380	gag Glu	act Thr	1272
	gca Ala	tca Ser	gat Asp 385	ctg Leu	ttg Leu	ctg Leu	cac His	tca Ser 390	gca Ala	ctg Leu	gtg Val	cag Gln	gag Glu 395	acc Thr	gcc Ala	tac Tyr	1320
	atc Ile	gaa Glu 400	gac Asp	cgg Arg	ccc Pro	ctg Leu	cat His 405	atg Met	ttg Leu	tac Tyr	tgt Cys	gct Ala 410	gcg Ala	gaa Glu	gag Glu	aac Asn	1368
	tgc Cys 415	ctg Leu	gcc Ala	agc Ser	tca Ser	gcc Ala 420	.cgc Arg	tca Ser	gcc Ala	aac Asn	tgg Trp 425	ccc Pro	tat Tyr	ggt Gly	cac His	cgg Arg 430	1416
	cgt Arg	ctg Leu	ctc Leu	cga Arg	ttc Phe 435	tcc Ser	tcc Ser	cag Gln	atc Ile	cac His 440	aac Asn	ctg Leu	gga Gly	cga Arg	gct Ala 445	gac Asp	1464
Harry days.	ttc Phe	agg Arg	ccc Pro	aag Lys 450	gct Ala	gly ggg	cgc Arg	cac His	tcc Ser 455	tgg Trp	gtg Val	tgg Trp	cac His	gag Glu 460	tgc Cys	cat His	1512
100 Jun 100 July 100	Gly 999	cat His	tac Tyr 465	cac His	agc Ser	atg Met	gac Asp	ttc Phe 470	ttc Phe	act Thr	cac His	tat. Tyr	gat Asp 475	atc Ile	ctc Leu	acc Thr	1560
Carl Han Birds	cca Pro	aat Asn 480	ggc Gly	acc Thr	aag Lys	gtg Val	gct Ala 485	gag Glu	ggc Gly	cac His	aaa Lys	gct Ala 490	agt Ser	ttc Phe	tgt Cys	ctc Leu	1608 (
III Hall Hall and	gaa Glu 495	gac Asp	act Thr	gag Glu	tgt Cys	cag Gln 500	gag Glu	gat Asp	gtc Val	tcc Ser	aag Lys 505	cgg Arg	tat Tyr	gag Glu	tgt Cys	gcc Ala 510	1656
Harry Land	aac Asn	ttt Phe	gga Gly	gag Glu	caa Gln 515	ggc Gly	atc Ile	act Thr	gtg Val	ggt Gly 520	tgc Cys	tgg Trp	gat Asp	ctc Leu	tac Tyr 525	cgg Arg	1704
	cat His	gac Asp	att Ile	gac Asp 530	tgt Cys	cag Gln	tgg Trp	att Ile	gac Asp 535	atc Ile	acg Thr	gat Asp	gtg Val	aag Lys 540	cca Pro	gga Gly	1752
	aac Asn	tac Tyr	att Ile 545	ctc Leu	cag Gln	gtt Val	gtc Val	atc Ile 550	aac Asn	cca Pro	aac Asn	ttt Phe	gaa Glu 555	gta Val	gca Ala	gag Glu	1800
	aqt	gac Asp 560	ttt Phe	acc Thr	aac Asn	aat Asn	gca Ala 565	atg Met	aaa Lys	tgt Cys	aac Asn	tgc Cys 570	Lys	tat Tyr	gat Asp	gga Gly	1848
	cat His 575	Arg	atc Ile	tgg Trp	gtg Val	cac His 580	aac Asn	tgc Cys	cac His	att Ile	ggt Gly 585	Asp	gcc Ala	ttc Phe	agt Ser	gaa Glu 590	1896
	gag Glu	gcc Ala	aac Asn	Arg	agg Arg 595	ttt Phe	gaa Glu	cgc Arg	tac Tyr	cct Pro 600	Gly	cag Gln	acc Thr	agc Ser	aac Asn 605	cag Gln	1944
		atc Ile	taa	gtgc	cac	tgcc	ctct	gc a	aacc	acca	c tg	gccc	ctaa	tgg	cagg	ggt	2000

ctgaggctgc	cattacctca	ggagcttacc	aagaaaccca	tgtcagcaac	cgcactcatc	2060
agaccatgca	ctatggatgt	ggaactgtca	agcagaagtt	ttcaccctcc	ticagaggcc	2120
agctgtcagt	atctgtagcc	aagcatggga	atctttgctc	ccaggcccag	caccgagcag	2180
aacagaccag	ageccaccac	accacaaaga	gcagcacctg	actaactgcc	cacaaaagat	2240
ggcagcagct	cattttcttt	aataggaggt	caggatggtc	agctccagta	tctcccctaa	2300
gtttaggggg	atacagettt	acctctagcc	ttttggtggg	ggaaaagatc	cagccctccc	2360
acctcatttt	ttactataat	atgttgctag	gtataatttt	attttatata	aaaagtgttt	2420
ctgtgattct	tcagagccca	ggagtcagtg	ctggtggttg	gagggacctg	ccccactgg	2480
ttcatttaac	cctctgtctc	ggtgccctca	gaacctcagc	cagaaaggca	aggaggaaat	2540
cagagcagga	gcctcatact	cttggtgatc	tattcattct	gtgacctcag	gggtcacata	2600
taaggtcagt	gtttctcgtc	cccgccggat	ctgcactgcc	aactgggatt	gggttcgaac	2660
agcttcataa	acatcttcag	cattttgtac	catctgctcc	ccaatggcca	aaatcacatc	2720
accaggccgc	agaccagccc	ggtgtgcagg	ggagcccagg	atgactttat	ggatgagtac	2780
accatgctga	acatcgggaa	agcttggttc	tcgaagctgt	agttcagcaa	ggatgctggg	2840
actcagggtc	agcatcatca	ccccaatgta	gegeegetgg	gacccactga	ttccggagga	2900
ggaattette	ttttccccac	gatgcagaaa	ctctcgaaga	cgatcagaag	ggatggcaaa	2960
ggagattcca	gctgtgacct	tcatggtgtt	cactccaatc	acctccccat	ccaggttaac	3020
caggggacct	ccagagtttc	caaaatcaat	agctgcatca	gtttgaatgt	attocacatt	3080
ggtttggggg	agtcccaggt	ctctggctgg	acgctgagca	gagctaacaa	tgccggatgt	3140
gatcgtgttc	tgcagtgcaa	agggacttcc	catggcaaca	acaaactccc	cetgeeggae	3200
atcagctgag	cgtcccagag	gcagcgtggg	gagaggetee	ttagtctgaa	tcctcagcgt	3260
tgcgatgtct	gccacgggat	ccacagctgt	gaccacggcc	tcatacgtgt	cgccgcttag	3320
cagtctcaca	cggactctgc	gccgatcagc	caccacatgg	gcgttggtga	caatgagccc	3380
atcggcagcc	accacgaatc	ctgagccgtt	cgagataggg	acctcgcggc	ccaagaaagg	3440
gtgccggtcc	aggatetega	tatagaccac	ggcaggtgct	gtcttctcca	ccacatctgc	3500
gatgaagttg	tactgactcc	ggggagaagc	gggcggcggg	ctagggacgg	cggcgaggac	3560
ggccggagga	ccccgacccc	cgccccacaa	caacaacagc	actgcccccc	cagegeeeag	3620
cgccaccgcc	agccacgcgc	gcgaacgggt	tccagagttc	tetgaggeet	cccgggtcct	3680
ggtatctggg	gtcaccgcag	tcagttgtgc	ccggggaccc	ggggtcccag	acgtcaggca	3740
tgctcggggt	tcagtgaccc	caacagacaa	ccgggcccag	agactggggg	tcccataagt	3800
cactcgggcc	cgggggtcag	aagttcctga	cgtcagcagg	gcccggaggt	caggggtcaa	3860
acggggtctc	ctcccccagc	gaatgccccc	caaagcccgc	catgcccgaa	ggctccagcc	3920

tgcaccccgc cccgccctcg gcgcagccat cagctccgcc ttggctgcct cctcgcccgc

	tccg	ggtg	jac t	gett	ccta	ic tg	ctc
Din 1	cctc	gtco	tg d	egaat	cttt	c to	ggg
had the trees were the trees that the trees th	<211 <212		08 PRT Iomo	sapi	ens		
	Met 1	Arg	Pro	Val	Ser 5	Val	Trp
	Cys	Leu	Leu	Суs 20	Ser	Ser	Cys
	Pro	Glu	Lys 35	Lys	Ala	Gly	Ser
	Phe	Pro	Arg	Lys	Pro	Tyr	Glu

115

cctactcaga ggcggcaccc aggacgcgag caggcggaca gtaggacgcg gggcacgccg 4040 gtacctgaag teetteagaa gtgeacgeeg ggaccaggat teegggagge egacteetee 4100 4160 ctgcccacg aatgccggga attgtggtct ccgccggacg cgagttgtga gacggcccaa ggggccgcgg ggtatgctgg gaccgctagc ccttccggcg cgcctcagga cttcgggtcc 4220 ceteaceceg ggeggatgee caaagactee geetteecaa gageecetge ggeegggege 4280 gaaaatggcg gcggcggcga .cggccgggcg ctcctgaagc agcagttatg gagcttccct 4340 cagggccggg gccggagcgg ctctttgact cgcaccggta agagacccgg cgggaagaga 4400 ccgatccccg cgtgctctcg gccttcggcg cctgaccact tcgcctctcg cccccaggct 4460 egtget getgetetae gegecagteg ygttetgeet 4520 4552 atcca cg o Gln Trp Ser Pro Trp Gly Leu Leu Leu s Leu Gly Ser Pro Ser Pro Ser Thr Gly r Gln Gly Leu Arg Phe Arg Leu Ala Gly u Gly Arg Val Glu Ile Gln Arg Ala Gly 50 Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly

120

	Lys 145	Asp	Gln	Arg	Leu	Pro 150	Gly	Phe	Ser	Asp	Ser 155	Asn	Val	Ile	Glu	Ala 160
	Arg	Val	Arg	Leu	Lys 165	Gly	Gly	Ala	His	Pro 170	Gly	Glu	Gly	Arg	Val 175	Glu
	Val	Leu	Lys	Ala 180	Ser	Thr	Trp	Gly	Thr 185	Val	Cys	Asp	Arg	Lys 190	Trp	Asp
	Leu	His	Ala 195	Ala	Ser	Val	Val	Cys 200	Arg	Glu	Leu	Gly	Phe 205	Gly	Ser	Ala
	Arg	Glu 210	Ala	Leu	Ser	Gly	Ala 215	Arg	Met	Gly	Gln	Gly 220	Met	Gly	Ala	Ile
drage from grap forth	His 225	Leu	Ser	Glu	Val	Arg 230	Cys	Ser	Gly	Gln	Glu 235	Leu	Ser	Leu	Trp	Lys 240
Half flat flat day	Cys	Pro	His	Lys	Asn 245	Ile	Thr	Ala	Glu	Asp 250	Cys	Ser	His	Ser	Gln 255	Asp
2 :	Ala	Gly	Val	Arg 260	Cys	Asn	Leu	Pro	Tyr 265	Thr	Gly	Ala	Glu	Thr 270	Arg	Ile
The state of the s	Arg	Leu	Ser 275	Gly	Gly	Arg	Ser	Gln 280	His	Glu	Gly	Arg	Val 285	Glu	Val	Gln
garie.	Ile	Gly 290	Gly	Pro	Gly	Pro	Leu 295	Arg	Trp	Gly	Leu	Ile 300	Cys	Gly	Asp	Asp
•	Trp 305	Gly	Thr	Leu	Glu	Ala 310	Met	Val	Ala	Cys	Arg 315	Gln	Leu	Gly	Leu	Gly 320
	Tyr	Ala	Asn	His	Gly 325	Leu	Gln	Glu	Thr	Trp 330	Туг	Trp	Asp	Ser	Gly 335	Asn
	Ile	Thr	Glu	Val 340	Val	Met	Ser	Gly	Val 345	Arg	Cys	Thr	Gly	Thr 350	Glu	Leu
	Ser	Leu	Asp 355		Cys	Ala	His	His 360		Thr	His	Ile	Thr		Lys	Arg
	Thr	Gly 370		Arg	Phe	Thr	Ala 375	Gly	Val	Ile	Cys	Ser 380		Thr	Ala	Ser

Asp Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile Glu 395 390

Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys Leu 410

Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg Leu 425

Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Fhe Arg 440 435

Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly His 450

Tyr His Ser Met Asp Phe Phe Thr His Tyr Asp Ile Leu Thr Pro Asn 475 470 465

Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu Asp 490 485

Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn Phe 500 505

Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His Asp 525 515

Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn Tyr 540 530

Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser Asp 550 545

Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His Arg

Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu Ala 585

Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile Ile 600

<210> 32

<211> 16545 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (862)..(14769)

<400> 32						
	ccccagaga	a aaacgctg	ed aat.tegt	tgc tttatt	gttc ectg	cctggg 60
gacctcaata	gccttttcc	a ttaacctt	cc cttctta	cgc aacggt	taat gact	ttgggg 120
gttgttttgc	tttctgttt	c tgctgagt	ca ctaaatt	ttg cctctt	tgtc coca	ggtgct 180
gctcagcata	aaagttaaa	a gtgcaatt	ca ggaagta	ctg ggattc	tgtg taga	gccgag 240
gaaaccattt	ccctaagag	a agctctgt	to attaget	tgt ccttcc	ttcc cggg	aaggaa 300
gcttccgagg	aacgaaggg	a gaagettt	gt tttgcct	gca gaagca	gece tgtg	ctcggc 360
tgagggttct	cagctggct	g tgaactgc	gg agdattg	tag gegeet	ggct ggct	caggcc 420
aatgcagaag	tctctccct	t ctccaaag	ac ccaaatc	ccc acagaa	ccag cttc	gagtta 480
ctttcccttc	aaggggatt	a aaataatt	gt gatttgt	ggc gctctc	cgtt cgcg	gtggta 540
ttttcctgtt	gtgttaaat	g cctcttat	ta agtaata	gat gtgatt	tatg tgaa	.cgacga 600
aggggtgtgt	ggtggattc	g gtgattaa	tc agtgaat	tcc catccg	ctgg catc	tctcac 660
tgcccctctt	gcgtgatgt	a agatcaga	cg taccetg	cat tgaaaa	gtca agac	acacgg 720
gcgtctcgct	cgcgctcac	a cacgetet	ga ataatat	ctc cagcac	gege geat	ccctcc 780
accttccaca	tcctgctcc	a ggcaggag	aa ggctgac	tgg ctggac	tcat tgag	ctgaag 840
aatttccagt	gacatttgt	a a atg acg Met Thi 1	-	ggt tcc ag Gly Ser Ar 5		
		gee gee ge Ala Ala Al				
ctc cag cg Leu Gln Ar		cct tac cg Pro Tyr Ar				
		ctc tcg gg Leu Ser Gl 50			a Arg Val	
		cga gat cae Arg Asp Gl: 65				
	s Asp His	gtg act tg Val Thr Cy 80				
		cct gat ga Pro Asp As				Cys
		atc aag tg Ile Lys Cy				

										tcc Ser									1275	
		_			~			_		gga Gly	_		_	_		-			1323	
				_		_	-		_	cag Gln			_		-		_		1371	
										gat Asp									1419	
	•		_	_	-		_			gaa Glu 195		_	~				_		1467	
										gga Gly									1515	
,										aac Asn									1563	
:		-			_	_				cta Leu			_			_			1611	
										agt Ser		_	_				tca Ser		1659	
į		_				-				ctg Leu 275	-						gat Asp		1707	
	-			_						gaa: Glu									1755	
	:	atc Ile	cag Gln 300	ata Ile	aca Thr	aaa Lys	gca Ala	gga Gly 305	gga Gly	tta Leu	aca Thr	gat Asp	gaa Glu 310	tgg Trp	aca Thr	atc Ile	aat Asn	٠.	1803	
	•									caa Gln									1851	
										cat His									1899	
										gtc Val 355									1947	
										gat Asp									1995	

											- 68	_						
						999 Gly												2043
						aca Thr												2091
						gac Asp 415												2139
						gtg Val												2187
•						ggc Gly												2235
			_	-		ttg Leu		_									_	2283
	the day day					ttt Phe												2331
	Control of the state of the sta					gga Gly 495												2379 (
,						gca Ala												2427
						tgt Cys												2475.
·		cgc Arg	tgc Cys 540	agg Arg	act Thr	ggc Gly	ttc Phe	aac Asn 545	ttg Leu	gga Gly	agt Ser	gat Asp	ggc Gly 550	agg Arg	tca Ser	tgc Cys	aaa Lys	2523
٠.						gag Glu												2571
			_	-	-	atg Met 575	_	_			-		_	_	_		_	2619
						aat Asn												2667
		_				atc Ile			_	_			_					2715
						gat Asp												2763

						gct Ala								2811
						agg Arg								2859
٠						aag Lys								2907
e. Ve.	cat His	_			 	gat Asp 690					_			2955
						ata Ile								3003
						aat Asn								3051
P. stand Benn Britt						act Thr								3099
m Call Par Arte						gat Asp						aat Asn		3147
			-	_		tac Tyr 770	_	 _		_			٠.	3195
						aat Asn								3243-
· .						gat Asp			_			_	٠,	3291
\$*·	ctg Leu					cta Leu								3339
						atg Met								3387
						cca Pro 850								3435
						aat Asn								3483
						tgt Cys								3531

	aac Asn	aga Arg	cac His	tgt Cys	atc Ile 895	caa Gln	gct Ala	cgg Arg	tgg Trp	aaa Lys 900	Cys	gat S Asp	ggo Gly	gac Asp	gat Asp 905	gac Asp	3579
	tgc Cys	cta Leu	gac Asp	gga Gly 910	agc Ser	gat Asp	gag Glu	gat Asp	tca Ser 915	Val	aac Asi	tgo n Cys	c tto s Pho	e aat e Asn 920	cat His	agc Ser	3627
	tgt Cys	cct Pro	gat Asp 925	gat Asp	cag Gln	ttt Phe	aaa Lys	tgc Cys 930	Gln	aat Asn	aat Asi	cge n Are	c tg g Cy: 93	c atc s Ile 5	ccc Pro	aag Lys	3675
,	aga Arg	tgg Trp 940	ctt Leu	tgt Cys	gat Asp	gga Gly	gct Ala 945	aat Asn	gac Asp	tgt Cys	gg Gl	g ag y Se: 95	r As	t gaa n Glu	gat Asp	gaa Glu	3723
	tcc Ser 955	aat Asn	caa Gln	act Thr	tgc Cys	aca Thr 960	gcc Ala	aga Arg	aca Thr	tgo Cys	ca Gl: 96	n. Va	a ga 1 As	c cag p Gln	ttt ?he	tct Ser 970	3771
a said desiry,	tgc Cys	gga Gly	aat Asn	ggg Gly	cgt Arg 975	tgc Cys	att Ile	ccc Pro	aga Arg	gca y Ala 980	Tr	g ct p Le	g tg u Cy	t gac s Asp	agg Arg 985	gaa Glu	3819
Cont for fresh	gac Asp	gac Asp	tgt Cys	ggt Gly 990	gac Asp	cag Gln	aca Thr	gat Asp	gaa Glu 995	ı Met	g gc E Al	a tc a Se	t tg r Cy	t gaa s Glu 100	Ph	c cca e Pro	3867
the state of the s			gag Glu 1005	Pr	a ct o Le	a ac u Th	c ca r Gl	n Ph	c c ie \	gta (/al (igc Cys	aaa Lys	agt Ser	gga Gly 1015	aga Arg		3912.
7.6 n.4	att Ile	agc Ser	agc Ser 1020	Ly	a tg s Tr	g ca p Hi	c tg s Cy	s As	ic t sp 5)25	ser i	gat Asp	gac Asp	gac Asp	tgt Cys 1030	gly ggg	gac Asp	3957
	ggg Gly	agt Ser	gat Asp 103!	Gl	g gt u Va	g gg 1 Gl	c to y Cy	rs Va	t d al I 040	cac His	tct Ser	tgc Cys	ttt Phe	gat Asp 1045	aat Asn		4002
			tgt Cys 105	Se 0	r Se	r Gl	y Ar	g Cy 10	/s :):5:5	Ile	Pro	Gly	His	tgg Trp 1060	gcc Ala	Cys	4047
	gat Asp	ggt Gly	gac Asp 106	As	t ga n As	c tg p Cy	jt gg 's Gl	y As	ac sp 070	ttc Phe	agt Ser	gat Asp	gaa Glu	gcc Ala 1075	cag Gln	atc Ile	4092
		_	act Thr 108	Ly	a ga 's Gl	a ga u Gl	ig at .u II	le H	at is : 085	tct Ser	cct Pro	gct Ala	ggt Gly	tgt Cys 1090	aac Asn	gga Gly	4137
			ttt Phe 109	Gl	ig t <u>g</u> .n Cy	rs Hi	ac co ls Pi	co A	at sp 100	ggt Gly	aat Asn	tgc Cys	gtt Val	cct Pro 1105	gat Asp	ttg Leu	4182
		-	tgt Cys 111	.As	it gg sp Gl	ja ga .y Gl	aa aa lu Ly		ac sp 115	tgt Cys	gaa Glu	gat Asp	ggt Gly	agt Ser 1120	gat Asp	gaa Gl.u	4227
			tgc Cys 112	As				le A		ttg Leu	tgt Cys	gac Asp	cac His	aaa Lys 1135	Thr	aag Lys	4272

		tcc Ser	tgt Cys 1140	tgg Trp	agt Ser	aca Thr	gly 999	aga Arg 1145	tgc Cys	atc Ile	aac Asn	aaa Lys	gca Ala 1150	tgg Trp	_ =	4317
	tgt Cys	gat Asp	gga Gly 1155	gat Asp	att Ile	gat Asp	tgc Cys	gaa Glu 1160	gat Asp	cag Gln	tca Ser	gat Asp	gaa Glu 1165	gat Asp	-	4362
	tgt Cys	gac Asp	agt Ser 1170	ttc Phe	ttg Leu	tgt Cys	gga Gly	cca Pro 1175	ccc Pro	aag Lys	cat His	cct Pro	tgt Cys 1180	gct Ala	aat Asn	4407
:	gac Asp	acc Thr	tca Ser 1185	gtc Val	tgc Cys	ctg Leu	cag Gln	cca Pro 1190	gag Glu	aaa Lys	ctc Leu	tgc Cys	aat Asn 1195	Gly 999		4452
i	-		tgt Cys 1200	cct Pro	gat Asp	ggc Gly	tct Ser	gat Asp 1205	gaa Glu	ggc Gly	tat Tyr	ctc Leu	tgt Cys 1210	gat Asp	gag Glu	4497
The state of the s	tgt Cys	tcg Ser	ctg Leu 1215	aac Asn	aat Asn	gga Gly	ggc Gly	tgt Cys 1220	agc Ser	aac Asn	cac His	tgt Cys	tct Ser 1225	gtt Val	gtt Val	4542
thing from July Herp ment them tent there	cct Pro	gga Gly	aga Arg 1230	gga Gly	att Ile	gtc Val	tgt Cys	tcc Ser 1235	Cys	cct Pro	gaa Glu	gga Gly	ctt Leu 1240	caa Gln	ctc Leu	4587
Call Prof. Sec.	aac Asn	aaa Lys	gac Asp 1245	aat Asn	aaa Lys	aca Thr	tgt Cys	gaa Glu 1250	att Ile	gtg Val	gat Asp	tat Tyr	tgt Cys 1255	agc Ser	aat Asn	4632
High state of	cat His	cta Leu	aag Lys 1260	tgc Cys	agc Ser	caa Gln	gta Val	tgt Cys 1265	Glu	cag Gln	cac His	aag Lys	cac His 1270	aca Thr	gtc Val	4677
	aag Lys	tgc Cys	tca Ser 1275	Cys	tat Tyr	gaa Glu	ggt ,Gly	tgg Trp 1280	Lys	ctg Leu	gat Asp	gta Val	gac Asp 1285	GIA	gaa Glu	4722
			aca Thr 1290	Ser	gtt Val	gat Asp	cct Pro	ttt Phe 1295	Glu	gca Ala	ttc Phe	atc Ile	atc Ile 1300	Phe	tct Ser	4767
		_	cat His 1305	Glu	atc Ile	aga Arg	agg Arg	att Ile 1310	Asp	ctt Leu	cac His	aaa Lys	aga Arg 1315	Asp	tat Tyr	4812
	agt Ser	cta Leu	ctt Leu 1320	Val	cct Pro	gga Gly	ttg Leu	aga Arg 1325	Asn	aca Thr	ata Ile	gca Ala	ctt Leu 1330	Asp	ttt Phe	4857
10 8 N	cac His	ttc Phe	aat Asn 1335	Gln	agt Ser	tta Leu	ctt Leu	tat Tyr 1340	Trp	aca Thr	gat Asp	gtt Val	gta Val 1.345	Glu	gac Asp	4902
	aga Arg	ata Ile	tac Tyr 1350	Arg	gga Gly	aag Lys	ctt Leu	tct Sér 1355	Glu	agt Ser	gga Gly	ggt Gly	gtc Val 1360	Ser	gcc Ala	4947
	att Ile	gaa Glu	gtg Val 1365	Val	gtg Val	gag Glu	cat His	ggc Gly 1370	Leu	gct Ala	act Thr	cca Pro	gaa Glu 1375	GΙΆ	ctg Leu	4992

	aca Thr	gtc Val	gac Asp 1380	tgg Trp	ata Ile	gca Ala	gga Gly	aac Asn 1385	ata Ile	tac Tyr	tgg Trp	ata Ile	gac Asp 1390	agc Ser	aat Asn	5037
	ctg Leu	gac Asp	caa Gln 1395	atc Ile	gaa Glu	gtg Val	gcc Ala	aaa Lys 1400	cta Leu	gat Asp	ggc Gly	tcc Ser	cta Leu 1405	aga Arg	act Thr	5082
	aca Thr	cta Leu	ata Ile 1410	gca Ala	gga Gly	gcc Ala	atg Met	gaa Glu 1415	cac His	ccc Pro	agg Arg	gcc Ala	att Ile 1420	gct Ala	ttg Leu	5127
		cca Pro	aga Arg 1425	tat Tyr	gga Gly	att Ile	ctt Leu	ttc Phe 1430	tgg Trp	aca Thr	gac Asp	tgg Trp	gat Asp 1435	gca Ala	aat Asn	5172
	ttt Phe	cct Pro	cgc Arg 1440	att Ile	gaa Glu	tct Ser	gcc Ala	tct Ser 1445	atg Met	agt Ser	ggt Gly	gct Ala	ggg Gly 1450	aga Arg	aaa Lys	5217
actor as an an according	acc Thr	atc Ile	tat Tyr 1455	aaa Lys	gac Asp	atg Met	aaa Lys	act Thr 1460	Gly 999	gct Ala	tgg Trp	cct Pro	aat Asn 1465	gga Cly	cta Leu	5262
chain their three first	act Thr	gtg Val	gac Asp 1470	cac His	ttt Phe	gag Glu	aaa Lys	agg Arg 1475	ata Ile	gtg Val	tgg Trp	aca Thr	gac Asp 1480	gcc Ala	agg Arg	5307
Call Proj. 10m.	tca Ser	gat Asp	gct Ala 1485	att Ile	tat Tyr	tca Ser	gcc Ala	ctc Leu 1490	Tyr	gat Asp	gga Gly	aca Thr	aac Asn 1495	Met	ata Ile	5352
	gaa Glu	atc Ile	atc Ile 1500	cga Arg	ggt Gly	cat His	gaa Glu	tac Tyr 1505	Leu	tcc Ser	cat His	ccc Pro	ttt Phe 1510	gct Ala	gtg Val	5397
771	tct Ser	cta Leu	tat Tyr 1515	gly 999	agt Ser	gaa Glu	gtc Val	tac Tyr 1520	Trp	aça Thr	gac Asp	tgg Trp	agg Arg 1525	Thr	aac Asn	5442. .*.
	aca Thr	ttg Leu	tcc Ser 1530	aaa Lys	gcc Ala	aat Asn	aag Lys	tgg Trp 1535	Thr	ggg Gly	cag Gln	aat Asn	gtc Val 1540	Ser	gtg Val	5487
			aaa Lys 1545	Thr	agt Ser	gca Ala	cag Gln	cca Pro 1550	Phe	gac Asp	ctt Leu	cag Gln	ata Ile 1555	Tyr	cat His	5532
	ccc Pro	agt Ser	cgc Arg 1560	cag Gln	cca Pro	cag Gl.n	gct Ala	ccc Pro 1565	Asn	cct Pro	tgt Cys	gca Ala	gct Ala 1570	Asn	gat Asp	5577
	ggc Gly	aaa Lys	ggc Gly 1575	Pro	tgc Cys	tct Ser	cac His	atg Met 1580	Cys	cta Leu	ato	aat Asn	cac His 1585	Asn	agg Arg	5622
	agt Ser	gct Ala	gcc Ala 1590	Cys	gcg Ala	tgc Cys	ccc	cac His 1595	Leu	atg Met	aag Lys	ctt Leu	tct Ser 1600	Ser	gac Asp	5667
			acc Thr 1605	Cys	tat Tyr	gaa Glu	atg Met	aaa Lys 1610	Lys				tat Tyr 1615	Alā	aga Arg	5712

	cgt Arg	tct Ser	gaa Glu 1620	atc Ile	aga Arg	gga Gly	gtg Val	gat Asp 1625	att 1]e	gac Asp	aat Asn	cca Pro	tac Tyr 1630	ttt Phe	aac Asn	5757
	ttc Phe	atc Ile	acg Thr 1635	gca Ala	ttt Phe	aca Thr	gtc Val	cct Pro 1640	gat Asp	att Ile	gat Asp	gac Asp	gtt Val 1645	act Thr	gtg Val	5802
	ata Ile	gac Asp	ttc Phe 1650	gat Asp	gca Ala	tct Ser	gag Glu	gaa Glu 1655	cgt Arg	tta Leu	tac Tyr	tgg Trp	aca Thr 1660	gat Asp		5847
	aaa Lys	Thr	caa Gln 1665	acc Thr	att Ile	aaa Lys	cga Arg	gct Ala 1670	ttt Phe	att Ile	aac Asn	gga Gly	act Thr 1675	999 Gly	tta Leu	5892
	gaa Glu	act Thr	gtt Val 1680	att Ile	tca Ser	aga Arg	gat Asp	att Ile 1685	cag Gln	agt Ser	atc Ile	aga Arg	999 Gly 1690	cta Leu	gca Ala	5937
	gtg Val	gat Asp	tgg Trp 1695	gtg Val	tca Ser	cgt Arg	aat Asn	tta Leu 1700	tac Tyr	tgg Trp	att Ile	agc Ser	tca Ser 1705	gaa Glu	ttt Phe	5982
Coli mag grand	gat Asp	gaa Glu	acg Thr 1710	caa Gln	att Ile	aat Asn	gtg Val	gca Ala 1715	agg Ærg	cta Leu	gat Asp	ggc Gly	tct Ser 1720	ttg Leu	aaa Lys	6027
Carl Bry Han	acc Thr	tca Ser	att Ile 1725	atc Ile	cat His	gga Gly	atc Ile	gat Asp 1730	aag Lys	cca Pro	cag Gln	tgt Cys	ctt Leu 1735	gca Ala	gct Ala	6072 -
m find the finds			gtc Val 1740	agg Arg	gga Gly	aaa Lys	ctc Leu	tac Tyr 1745	Trp	acc Thr	gat Asp	gga Gly	aac Asn 1750	aca Thr	att Ile	6117
Hall Hall all.	aac Asn	atg Met	gca Ala 1755	aat Asn	atg Met	gat Asp	ggc	agt Ser 1760	Asn	agc Ser	aag Lys	att Ile	ctg Leu 1765	ttt Phe	cag Gln	6162
	aat Asn	cag Gl'n	aag Lys 1770	gag Glu	cca Pro	gtt Val	ggt Gly	cta Leu 1775	Ser	ata Ile	gac Asp	tat Tyr	gtg Val 1780	Glu	aac Asn	6207
	_		tat Tyr 1785	Trp	atc Ile	agt Ser	tcg Ser	999 Gly 1790	Asn	gga Gly	acc Thr	ata Ile	aat Asn 1795	Arg	tgc Cys	6252
		ctg Leu		ggt Gly	ggt Gly	aat Asn	tta Leu	gaa Glu 1805	Val	atc Ile	gag Glu	tca Ser	atg Met 1810	Lys	gaa Glu	6297
			aca Thr 1815	Lys	gct Ala	aca Thr	gcc Ala	cta Leu 1820	Thr				aag Lys 1825	Lya	ctg Leu	6342
			gca Ala 1830	Asp	caa Gln	aac Asn	tta Leu	gc.c Ala 1835	Glr				tgc Cys 1840	Sei	aaa Lys	6387
	_	_	gga Gly 1845	Arg				atc Ile 1850	Let				act Thr 1855	Ser	ggg Gly	6432

	gta Val	Val	cat His 1860	atg Met	aaa Lys	gtc Val	tat Tyr	gat Asp 1865	aaa Lys	gaa Glu	gca Ala	cag Gln	caa Gln 1870	ggc	agc Ser	6477
	aat Asn	tcc Ser	tgc Cys 1875	caa Gln	cta Leu	aac Asn	aat Asn	ggt Gly 1880	gga Gly	tgc Cys	tct Ser	caa Gln	ctt Leu 1885	tgt Cys	tta Leu	6522
	cca Pro	aca Thr	tct Ser 1890	gaa Glu	act Thr	aca Thr	agg Arg	act Thr 1895	tgt Cys	atg Met	tgt Cys	aca Thr	gtg Val 1900	gga Gly	tat Tyr	6567
٠.	tat Tyr	ctc Leu	caa Gln 1905	aag Lys	aac Asn	cgt Arg	atg Met	tca Ser 1910	tgt Cys	caa Gln	ggt Gly	ata. Ile	gaa Glu 1915	tca Ser	ttt Phe	6612
	ctt Leu	atg Met	tac Tyr 1920	tct Ser	gtt Val	cat His	gaa Glu	gga Gly 1925	atc Ile	agg Arg	gga Gly	ata Ile	cct Pro 1930	ctt Leu	gaa Glu	6657
Jung, Hands	cca Pro	agt Ser	gac Asp 1935	aaa Lys	atg Met	gat Asp	gct Ala	ttg Leu 1940	Met	cct Pro	ata Ile	tca Ser	gga Gly 1945	act Thr	tca Ser	6702
men jene gan jene jene men jene	ttt Phe	gcc Ala	gtģ Val 1950	gga Gly	ata Ile	gat Asp	ttc Phe	cat His 1955	gca Ala	gaa Glu	aat Asn	gat Asp	acc Thr 1960	atc Ile	tac Tyr	6747
fail for free	tgg Trp	aca Thr	gac Asp 1965	atg Met	ggc Gly	ttc Phe	aat Asn	aaa Lys 1970	at.t Ile	agc Ser	aga Arg	gct Ala	aaa Lys 1975	aga Arg	gat Asp	6792 -
in the control of the	cag Gln	act Thr	tgg Trp 1980	Lys	gaa Glu	gat Asp	atc Ile	att Ile 1985	Thr	aat Asn	ggc Gly	t.tg Leu	gga Gly 1990	aga Arg	gtg Val	6837
. I will start in the start ind	gaa Glu	ggg Gly	ata Ile 1995	Ala	gtt Val	gac Asp	tgg Trp	att Ile 2000	gct Ala	ggt Gly	aac Asn	ata Ile	tat Tyr 2005	Trp	aca Thr	6882,
	gat Asp	cat His	ggt Gly 2010	Phe	aac Asn	tta Leu	att Ile	gaa Glu 2015	Val	gca Ala	aga Arg	ctc Leu	aat Asn 2020	Gly	tct Ser	6927
	ttc Phe	cgt Arg	tat Tyr 2025	Val	att Ile	att Ile	tcc Ser	caa Gln 2030	Gly	ctg Leu	gat Asp	caa Gln	cca Pro 2035	Arg	tct Ser	6972
	ata Ile	gct Ala	gtg Val 2040	His	cca Pro	gag Glu	aaa Lys	ggc Gly 2045	Leu	ttg Leu	ttc Phe	tgg Trp	act Thr 2050	GLu	tgg Trp	7017
	gga Gly	caa Gln	atg Met 2055	Pr.o	tgt Cys	att Ile	gga Gly	aag Lys 2060	Ala	cgc Arg	ttg Leu	gat Asp	ggc Gly 2065	Ser	gag Glu	7062
			gtc Val 2070	Leu				gga Gly 2075	Ile	gca Ala	tgg Trp	ccg Pro	aat Asn 2080	Gly	atc Ile	7107
			gac Asp 2085	Tyr	gag Glu	gaa Glu	aat Asn	aaa Lys 2090	Leu	tac Tyr	tgg Trp	tgt Cys	gat Asp 2095	Ala	cgc Arg	7152

	aca Thr	gac Asp	aag Lys 2100	ata Ile	gag Glu	aga Arg	atc Ile	gac Asp 2105	ctt Leu	gag Glu	act Thr	gga Gly	ggg Gly 2110	aat Asn	cgc Arg	7197
	gag Glu	atg Met	gtg Val 2115	ctg Leu	tca Ser	gga Gly	agc Ser	aat Asn 2120	gtg Val	gat Asp	atg Met	ttt Phe	tca Ser 2125	gtt Val	gca Ala	7242
	gtc Val	ttt Phe	999 Gly 2130	gct Ala	tac Tyr	atc Ile	tac Tyr	tgg Trp 2135	tct Ser	gac Asp	aga Arg	gca Ala	cat His 2140	gca Ala	aac Asn	7287
	ggg Gly	tct Ser	gtc Val 2145	aga Arg	agg Arg	ggc Gly	cac	aag Lys 2150	aat Asn	gat Asp	gcc Ala	aca Thr	gaa Glu 2155	acg Thr	ata Ile	7332
	acc Thr	atg Met	aga Arg 2160	acc Thr	ggc Gly	ctt Leu	gga Gly	gtc Val 2165	aac Asn	ctg Leu	aag Lys	gag Glu	grt Val 2170	aaa Lys	ata Ile	7377
	ttt Phe	aac Asn	cga Arg 2175	.gta Val	aga Arg	gag Glu	aaa Lys	999 Gly 2180	acc Thr	aat Asn	gtt Val	tgt Cys	gcc Ala 2185	agg Arg	gac Asp	7422
den jan gal, gan and som sor hat	aat Asn	ggt Gly	ggc Gly 2190	Cys	aag Lys	caa Gln	ctc Leu	tgt Cys 2195	ctt Leu	tat Tyr	çga Arg	gga Gly	aat Asn 2200	tcc .Ser	cgg Arg	7467
Hall Bird Bern	aga Arg	act Thr	tgt Cys 2205	gct Ala	tgt Cys	gcc Ala	cat His	gga Gly 2210	Tyr	ttg Leu	gca Ala	gaa Glu	gat Asp 2215	gga Gly	gtt Val	7512
The state of the s	act Thr	tgc Cys	ctg Leu 2220	Arg	cat His	gaa Glu	ggc Gly	tat Tyr 2225	Leu	Leu	tat Tyr	tca Ser	gga Gly 2230	aga Arg	aca Thr	7557
	ata Ile	tta Leu	aaa Lys 2235	Ser	ata Ile	cat His	ctt Leu	tct Ser 2240	Asp	gaa Glu	acc Thr	aat Asn	tta Leu 2245	Asn	tcc Ser	7602
 ·	cca Pro	ața Ile	agg Arg 2250	Pro	tat Tyr	gag Glu	aat Asn	cca Pro 2255	Arg	tat Tyr	ttc Phe	aag Lys	aat Asn 2260	Va L	ata Ile	7647
	gcc Ala	ttg Leu	gct Ala 2265	Phe	gac Asp	tat Tyr	aat Asn	caa Gln 2270	Arg	aga Arg	aaa Lys	ggt Gly		aac Asn		7692
			tac Tyr 2280	Ser	gat Asp	gca Ala	cac His	ttt Phe 2285	Gly	aat Asn	ata Ile	cag Gln	ctt Leu 2290	I.l.e	aaa Lys	7737
	gac Asp	aac Asn	tgg Trp 2295	Glu	gac Asp	aga Arg	caa Gln	gta Val 2300	Ile	gtt Val	gaa Glu	. aat . Asn	gtg Val 2305	GLy	tct Ser	7782
	gt <u>c</u> Val	ggaa Glu	gga Gly 2310	Leu	gcc Ala	tat Tyr	cac His	aga Arg 2315	Ala	tgg Trp	gat Asp	aca Thr	ctg Leu 2320	Tyr	tgg Trp	7827
		_	tct Ser 2325	Thr	acc Thr	tca Ser	tcc Ser	atc Ile 2330	Thr	aga Arg	cac His	act Thr	gtg Val 2335	Asp	cag Gln	7872

,	act Thr	cgg Arg	cct Pro 2340	gga Gly	gca Ala	ttt Phe	gac Asp	agg Arg 2345	gaa Glu	gct Ala	gtc Val	atc Ile	acc Thr 2350	atg Met	tca Ser		7917
•	gaa Glu	gat Asp	gac Asp 2355	cat His	cca Pro	cat His	Val	cta Leu 2360	ycc Ala	ttg Leu	gat Asp	gaa Glu	tgt Cys 2365	caa Gln	aat Asn		7962
			ttt Phe 2370	tgg Trp	acc Thr	aac Asn	tgg Trp	aat Asn 2375	gaa Glu	caa Gln	cat His	cca Pro	agt Ser 2380	atc ile	atg Met		8007
	aga Arg	tct Ser	act Thr 2385	ctg Leu	act Thr	gly ggg	aaa Lys	aat Asn 2390	gct Ala	caa Gln	gtg Val	gtg Val	gtc Val 2395	agt Ser	aca Thr		8052
			ctc Leu 2400	act Thr	cca Pro	aat Asn	gga Gly	ctt Leu 2405	act Thr	atc Ile	gac Asp	tac Tyr	cgt Arg 2410	gca Ala	gag Glu		8097
			tat Tyr 2415	ttc Phe	tca Ser	gat Asp	ggc Gly	agt Ser 2420	cta Leu	gga Gly	aaa Lys	att Ile	gaa Glu 2425	agg Arg	tgt Cys		8142
	gaa Glu	tac Tyr	gat Asp 2430	gga Gly	tcc Ser	cag Gln	aga Arg	cat His 2435	gtg Val	ata Ile	gtt Val	aaa Lys	tct Ser 2440	ggg Gly	cca Pro		8187
	ggg Gly	act Thr	ttc Phe 2445	ctc Leu	agt Ser	ttg Leu	gct Ala	gtt Val 2450	tat Tyr	gac Asp	aat Asn	tat Tyr	ata Ile 2455	ttc Phe	tgg Trp		.8232 ₁
	tcg. Ser	gac Asp	tgg Trp 2460	Gly	aga Arg	aga Arg	gct Ala	ata Ile 2465	ctg Leu	cgg Arg	tcc Ser	aac Asn	aag Lys 2470	tac Tyr	aca Thr		8277
	gga Gly	gga Gly	gat Asp 2475	Thr	aaa Lys	att Ile	ctt Leu	cgt Arg 2480	Ser	gat Asp	att Ile	cca Pro	cat His 2485	cag Gln	cca Pro		8322 <u>:</u>
	atg Met	gga Gly	atc Ile 2490	Ile	gct Ala	gtt Val	gcc Ala	aat Asn 2495	Asp	acc Thr	aat Asn	agc Ser	tgt Cys 2500	G!u	ctt Leu	,	8367.
	tct Ser	cca Pro	tgt Cys 2505	Ala	tta Leu	ttg Leu	aat Asn	gga Gly 2510	Gly	tgc Cys	cat His	gac Asp	ttg Leu 2515	Cys	ctt Leu		8412
	tta Leu	act Thr	ccc Pro 2520	Asn	ggg ggg	aga Arg	gtg Val	aat Asn 2525	Cys	tcc Ser	tgc Cys	aga Arg	ggg Gly 2530	Asp	cga Arg		8457
	ata Ile	ttg Leu	cta Leu 2535	Glu	gac Asp	aac Asn	aga Arg	tgt Cys 2540	Val	act Thr	aaa Lys	aat Asn	tcc Ser 2545	Ser	tgc Cys		8502
	aac Asn	Ala	tat Tyr 2550	Ser	gag Glu	ttt Phe	gaa Glu	tgt Cys 2555	Gly	aat Asn	ggt Gly	gag Glu	tgc Cys 2560	Tite	gac Asp		8547
	tac Tyr	cag Glr	ctc Leu 2565	Thr	tgt Cys	gat Asp	ggc Gly	att Ile 2570	Pro	cac His	tgt Cys	aaa Lys	gat Asp 2575	Lys	tca Ser		8592

And the first and the first the firs

		gat Asp	gaa Glu	aaa Lys 2580	ctg Leu	ctc Leu	tac Tyr	tgt Cys	gaa Glu 2585	aac Asn	aga Arg	agc Ser	tgt Cys	cga Arg 2590	aga Arg	ggc Gly		8637
		ttc Phe	aag Lys	cca Pro 2595	tgc Cys	tat Tyr	aat Asn	cgc Arg	cgc Arg 2600	tgc Cys	att Ile	cct Pro	cat His	ggc Gly 2605	aag Lys			8682
		tgt Cys	gat Asp	gga Gly 2610	gaa Glu	aat Asn	gac Asp	tgc Cys	gga Gly 2615	gac Asp	aac Asn	tct Ser	gat Asp	gaa Glu 2620	tta Leu	gat Asp		8727
		tgt Cys	aaa Lys	gtt Val 2625	tca Ser	acc Thr	tgt Cys	gcc Ala	acg Thr 2630	gtt Val	gag Glu	ttc Phe	cgc Arg	tgt Cys 2635	gca Ala	gat Asp		8772
	•	gly aaa	act Thr	tgt Cys 2640	att Ile	cca Pro	aga Arg	tca Ser	gca Ala 2645	cga Arg	tgc Cys	aac Asn	cag Gln	aac Asn 2650	ata .Ile	gat Asp		8817
		tgt Cys	gca Ala	gat Asp 2655	gct Ala	tca Ser	gat Asp	gaa Glu	aag Lys 2660	aac Asn	t.gc Cys	aat Asn	aac Asn	aca Thr 2665	gac Asp	tgc Cys		8862
there there there there	v	aca Thr	cat His	ttc Phe 2670	tat Tyr	aag Lys	ctt Leu	gga Gly	gtg Val 2675	lys	acc Thr	aca Thr	ggg Gly	ttc Phe 2680		aga Arg	•	8907
the state of the s				tct Ser 2685	acc Thr	tca Ser	ctg Leu	tgt Cys	gtt Val 2690	ctg Leu	cca Pro	acc Thr	tgg Trp	ata Ile 2695	tgc Cys	gac Asp		8952 <u>.</u> ;
# ## ##		ggg Gly	tct Ser	aat Asn 2700	gac Asp	tgt Cys	gga Gly	gac Asp	tat Tyr 2705	Ser	gat Asp	gaa Glu	tta Leu	aag Lys 2710	tgc Cys	cca Pro		8997
The first that the	:	gtt Val	cag Gln	aac Asn 2715	aaa Lys	cac His	aaa Lys	tgt Cys	gaa Glu 2720	Glu	aat Asn	tat Tyr	ttt Phe	agt Ser 2725	. tgt . Cys	cct Pro		9042
				aga Arg 2730	tgc Cys	att Ile	ttg Leu	aat Asn	acc Thr 2735	Trp	ata Ile	tgc Cys	gat Asp	ggt Gly 2740	GIn	.aaa Lys		9087
-		_	_	gag Glu 2745	Asp	gga Gly	cgt Arg	gat Asp	gaa Glu 2750	Phe	cac	tgt Cys	gat Asp	tct Ser 2755	Ser	tgc Cys		9132
,				aac Asn 2760					tcc Ser 2765	Ala				att Ile 2770	Ser	. aag Lys		9177
				att Ile 2775	Cys				gat Asp 2780	Asp	tgt Cys	ggg	gat Asp	999 Gly 2785	Let	gat Asp		9222
				gac Asp 2790	Ser				gcc Ala 2795	Ile				gct Ala 2800	Āsp	atg Met		9267
			_	tgc Cys 2805	Gln				gcc Ala 2810	Cys				cat His 2815	Trp	g ctt Leu		9312

										- /	8 -								
				ggt Gly 2820												tcc Ser		9357	
				ggc Gly 2835														9402	
		_	-	cat His 2850				_			_			_	tgt Cys	_		9447	
	:.			gac Asp 2865														9492	
	-1			cga Arg 2880													,	9537	
•	And the state of t			ctt Leu 2895														9582	
	the form the factor of the fac			gac Asp 2910														9627	
	Toole done done	agt Ser	gca Ala	gaa Glu 2925	cag Gln	tca Ser	tgc Cys	aac Asn	agt Ser 2930	tca Ser	ttt Phe	ttt Phe	atg Met	tgc Cys 2935	aaa Lys	aat Asn		9672.	
	T. H. H. J.	ggc Gly	agg Arg	tgc Cys 2940	att Ile	ccc Pro	agt Ser	gga Gly	ggt Gly 2945	ctt Leu	tgt Cys	gac Asp	aat Asn	aag Lys 2950	gat Asp	gac Asp		9717	
	The Hole and			gat Asp 2955														9762 _{5.}	
٠.	œ.			aag Lys 2970														9807	
		_	gtc Val	agt Ser 2985										caa Gln 2995				9852	
		gat Asp	gac Asp	ggc Gly 3000	aaa Lys	aca Thr	tgt Cys	gta Val	gac Asp 3005	att Ile	gat Asp	gaa Glu	tgc Cys	tct Ser 3010	tca Ser	ggc Gly		9897	
	;	ttt Phe	ccc Pro	tgt Cys 3015	agc Ser	cag Gln	caa Gln	tgc Cys	atc Ile 3020	aat Asn	aca Thr	tac Tyr	ggg Gly	act Thr 3025	tac Tyr	_		9942	
		_	ctc Leu	tgt Cys 3030					_				_	aac Asn 3040				9987	
				aaa Lys 3045										att Ile 3055				10032	

	gat Asp	cat His	cat His 3060	gag Glu	ata Ile	agg Arg	aaa Lys	att Ile 3065	agc Ser	act Thr	gat Asp	ggc Gly	tcc Ser 3070	aac Asn	tac Tyr		10077
	aca Thr	ctt Leu	tta Leu 3075	aaa Lys	cag Gln	gga Gly	tta Leu	aac Asn 3080	aat Asn	gtt Val	att Ile	gct Ala	ata Ile 3085	gac Asp	ttt Phe		10122
;	gat Asp	tac Tyr	aga Arg 3090	gaa Glu	gaa Glu	ttc Phe	atc Ile	tat Tyr 3095	tgg Trp	atc	gat Asp	tct Ser	agc Ser 3100	cga Arg	ccc Pro		10167
٠,	aat Asn	ggc Gly	agt Ser 3105	cgc Arg	ata Ile	aat Asn	aga Arg	atg Met 3110	tgt Cys	tta Leu	aat Asn	gga Gly	agt Ser 3115	gac Asp	att Ile		10212
Ý.	aag Lys	gta Val	gtt Val 3120	cat His	aac Asn	aca Thr	gcg Ala	gtc Val 3125	Pro	aat Asn	gca Ala	ctt Leu	gct Ala 3130	gtc Val	gat Asp		10257
Fr. Th.	tgg Trp	att Ile	gga Gly 3135	aaa Lys	aac Asn	ctc Leu	tat Tyr	tgg Trp 3140	tct Ser	gac Asp	aca Thr	gaa Glu	aaa Lys 3145		atc Ile		10302
A period from the state of the	att Ile	gaa Glu	gta Val 3150	Ser	aaa Lys	ctc Leu	aat Asn	ggc Gly 3155	ttg Leu	tac Tyr	cct Pro	act Thr	ata Ile 3160		gtt Val	٠	10347
that the after	agc Ser	aaa Lys	agg Arg 3165	ctg Leu	aag Lys	ttt Phe	ccc Pro	aga Arg 3170	gac Asp	ttg Leu	t.ct Ser	tta Leu	gat Asp 3175	Pro	caa Gln		10392
te full before	gct Ala	gga Gly	tat Tyr 3180	Leu	tat Tyr	tgg Trp	att Ile	gac Asp 3185	tgc Cys	tgc Cys	gag Glu	tat Tyr	cct Pro 3190	His	att Ile		10437
	ggc Gly	cgt Arg	gtt Val 3195	Gly	atg Met	gat Asp	gga Gly	acc Thr 3200	Asn	¢ag Gln	agt Ser	gtt Val	gtc Val 3205	lle	gaa Glu		10482-
	acc Thr	aag Lys	att Ile 3210	Ser	aga Arg	cct Pro	atg Met	gca Ala 3215	Leu	aca Thr	ata Ile	gat Asp	tat Tyr 3220	Val	aat Asn		10527
			ctc Leu 3225	Tyr	tgg Trp	gcc Ala	gat Asp	gaa Glu 3230	Asn	cac His	att Ile	gaa Glu	ttt Phe 3235	ser	aac Asn		10572
			gga Gly 3240	Ser	cat His	aga Arg	cac His	aaa Lys 3245	Val	cct Pro	aat Asr	caa Gln	gat Asp 3250	Ile	. cca Pro		1.0617
: ./	Gly 999	gtg Val	att Ile 3255	Ala	cta Leu	aca Thr	ttg Leu	ttt Phe 3260	Glu	gac Asp	tac Tyr	ato Ile	tac Tyr 3265	Tr	act Thr		10662
	_		aaa Lys 3270	Thr	aag Lys	tca Ser	cto Leu	agc Ser 3275	Arg	gcc	cat His	aaa Lys	aca Thr 3280	Ser	gga Gly		10707
	_	_	aga Arg 3285	Leu				tac Tyr 3290	Ser	tgg Trp	g cat His	gcc Ala	atc Ile 3295	Thi	gat Asp		10752

		-	gtg Val 3300			aga Arg 3305			_	_			cat His	10797
			atg Met 3315			ggt Gly 3320							tta Leu	10842
	-					tgt Cys 3335	-	_					tat Tyr	10867
						tga Cys 3350							agc Ser	10932
· .						aaa Lys 3365							aaa Lys	10977
Man Wall						ggt Gly 3380							gat Asp	11022
then then then the						cag Gln 3395							gly aaa	11067
the first that						gct Ala 3410							aat Asn	11112:
II. II. II. II. II. II. II. II. II.						gaa Glu 3425								· 11157
						tgt Cys 3440		_		_	aaa Lys 3445	_	atc Ile	11202
		gta Val				999 Gly 3455							gag Glu	11247
						gaa Glu 3470								11292
						cat His 3485								11337
						gca Ala 3500								11382
		-		_	-	 cct Pro 3515		_		_	4.0			11427
			tgt Cys 3525			tgg Trp 3530					caa Gln 3535	aat Asn	-	11472

	_	agt Ser	_			_	_	gaa Glu 3545		_	_		_	aca Thr	_	11517
		_	aaa Lys 3555	_			_	gcc Ala 3560			_	_	gtt Val 3565	tct Ser	tca Ser	11562
		ttt Phe						ttt Phe 3575							gat Asp	11607
		aga Arg						tgt Cys 3590						cgg Arg	_	11652
				_	_			gca Ala 3605					gat Asp 3610	ggc Gly		11697
Application of the state of the	-	_	tgc Cys 3615					gat Asp 3620					gag Glu 3625	cca Pro		11742
Heart Street Str		cct Pro	act Thr 3630					gaa Glu 3635					agt Ser 3640	gat Asp	gga Gly	11787
The state of the s	_		tca Ser 3645	-		_		tgt Cys 3650			_		gat Asp 3655	tgt Cys		11832
or the sheet that the	-		tca Ser 3660					tgt Cys 3665						gaa Glu	_	11877
		ttt Phe	cgg Arg 3675					gcc Ala 3680						aga Arg		11922
								tgt Cys 3695					gat Asp 3700	_	gag Glu	11967
		tgt Cys		aga Arg	gga Gly	gga Gly	aat Asn	ata Ile 3710	tgt Cys	aga Arg	gct Ala	gat Asp	gag Glu 3715		ctt Leu	12012
	_	aat Asn	aat Asn 3720					cta Leu 3725					tgt Cys 3730	_	gga Gly	12057
-		_	_	_		-		tct Ser 3740					gat Asp 3745	atg Met	•	12102
	-	aaa Lys	ttt Phe 3750		_			acg Thr 3755					tgc Cys 3760	aga Arg	aat Asn	12147
		aga Arg						gag Glu 3770		_	_		999 Gly 3775	att Ile	gat Asp	12192

gaa Glu	tgc Cys	ggt Gly 3780	gac Asp	aat Asn	tca Ser	gat Asp	gaa Glu 3785	gat Asp	cac His	tgt Cys	ggt Gly	ggt Gly 3790	aag Lys	ctg Leu	12237
	tat Tyr	aaa Lys 3795	gca Ala	agg Arg	cct Pro	tgt Cys	aaa Lys 3800	aag Lys	gat Asp	gag Glu	ttt Phe	gct Ala 3805	tgt Cys	agt Ser	12282
aat Asn	aaa Lys	aaa Lys 3810	tgc Cys	atc Ile	cct Pro	atg Met	gat Asp 3815	ctc Leu	cag Gln	tgt Cys	gat Asp	cga Arg 3820	ctt Leu	gat Asp	12327
gac Asp	tgc Cys	gga Gly 3825	gat Asp	ggt Gly	tca Ser	gat Asp	gag Glu 3830	caa Gln	gga Gly	tgc Cys	aga Arg	ata Ile 3835	gct Ala	cct Pro	12372
	gaa Glu	tat Tyr 3840	acc Thr	tgt Cys	gaa Glu	gat Asp	aat Asn 3845	gtg Val	aat Asn	cca Pro	tgt Cys	gga Gly 3850	gat Asp	gat Asp	12417
gca Ala	tat Tyr	tgt Cys 3855	aat Asn	caa Gln	ata Ile	aaa Lys	aca Thr 3860	tct Ser	gtt Val	ttc Phe	tgt Cys	cgc Arg 3865	tgt Cys	aag Lys	12462
		ttt Phe 3870					aaa Lys 3875	aac Asn	aga Arg	caa Gln	tgt Cys	gaa Glu 3880	gac Asp	ctt Leu	12507
aat Asr	gaa Glu	tgt Cys 3885	ttg Leu	gtg Val	ttt Phe	ggc Gly	aca Thr 3890	tgt Cys	tcc Ser	cat His	caa Gln	tgt Cys 3895	ata Ile	aat Asn	12552
gtç Va]	gaa Glu	gga Gly 3900	tca Ser	tat Tyr	aaa Lys	tgt Cys	gtg Val 3905	tgt Cys	gac Asp	cag Gln	aat Asn	ttt Phe 3910	caa Gln	gaa Glu	12597
		aac Asn 3915	Thr	tgc Cys	ata Ile	gca Ala	gaa Glu 3920	Gly	tct Ser	gaa Glu	gat Asp	caa Gln 3925	gtt Val	ctc Leu	12642
tac Tyi	att Ile	gct Ala 3930	Asn	gac Asp	act Thr	gat Asp	atc Ile 3935	Leu	ggt Gly	ttt Phe	ata Ile	tat Tyr 3940	Pro	ttc Phe	12687
aa(Ası	tac 1 Tyr	agt Ser 3945	Gly	gat Asp	cat His	caa Gln	caa Gln 3950	Ile	tct Ser	cat His	att Ile	gaa Glu 3955	His	aat Asn	12732
tca Sei	a aga Arg	ata Ile 3960	Thr	Gly aaa	atg Met	gat Asp	gta Val 3965	Tyr	tat Tyr	caa Gln	aga Arg	gat Asp 3970	Met	att Ile	12777
		agt Ser 3975	Thr	cag Gln	ttt Phe	aat Asn	cca Pro 3980	Gly	gga Gly	att Ile	ttc Phe	tac Tyr 3985	Lys	agg Arg	12822
ate Ile	c cat e His	ggc Gly 3990	Arg	gaa Glu	aaa Lys	agg Arg	caa Gln 3995	Ala	aac Asn	agt Ser	ggc Gly	ttg Leu 4000	Ile	tgt Cys	12867
cc Pro	t gaa o Glu	ttt Phe 4005	Lys	agg Arg	ccc	agg Arg	gac Asp 4010	Ile	gca Ala	gtt Val	gac Asp	tgg Trp 4015	Val	gct Ala	12912

" " " " " " " " " " " " " " " " " " "	7
	11111
ũ	1
1	1
1	1000
tal Mar Mar	Trees.
4	17.00
ũ	
ž	
-	
-	-
Allen allen	
The sheet	
F	
F	
į	

		att Ile 4020	tac Tyr	tgg Trp	act Thr	gat Asp	cat His 4025	tct Ser	aga Arg	atg Met	cat His	tgg Trp 4030	ttc Phe		12957
	-	act Thr 4035	act Thr	cac His	tgg Trp	acc Thr	agt Ser 4040	ctg Leu	agg Arg	tac Tyr	tct Ser	atc Ile 4045	aac Asn	_	13002
	cag Gln	ctg Leu 4050	aat Asn	ggc Gly	ccc Pro	aac Asn	tgc Cys 4055	acc Thr	aga Arg	ctc Leu	tta Leu	aca Thr 4060	aat Asn	_	13047
gct Ala	gga Gly	gaa Glu 4065	ccc Pro	tat Tyr	gct Ala	att Ile	gca Ala 4070	gta Val	aat Asn	cct Pro	aaa Lys	aga Arg 4075	gjà aaa	_	13092
_		tgg Trp 4080	act Thr	gtt Val	gtt Val	999 Gly	gat Asp 4085	cat His	tcc Ser	cat His	ata Ile	gaa Glu 4090	_	gca Ala	13137
_		gat Asp 4095	ggt Gly	aca Thr	ctg Leu	aga Arg	agg Arg 4100	att Ile	tta Leu	gta Val	caa Gln	aag Lys 4105		tta Leu	13182
	-	ccc Pro 4110	aca Thr	ggt Gly	ttg Leu	gct Ala	gtg Val 4115	gat Asp	tat Tyr	ttt Phe	agt Ser	gaa Glu 4120		ata Ile	13227
		gct Ala 4125	gac Asp	ttt Phe	gag Glu	ctc Leu	tcc Ser 4130	atc Ile	att Ile	ggc Gly	agt Ser	gtt Val 4135	ctg Leu	tat Tyr	13272
		tct Ser 4140	aat Asn	tca Ser	gta Val	gtc Val	tct Ser 4145	gtc Val	agc Ser	agc Ser	aaa Lys	caa Gln 4150	ggt Gly	tta Leu	13317
tta Leu	cat His	cca Pro 4155	cat His	agg Arg	atc Ile	gat Asp	atc Ile 4160	Phe	gaa Glu	gat Asp	tat Tyr	ata Ile 4165	tat Tyr	gga Gly	13362
_		cct Pro 4170	aaa Lys	aat Asn	ggt Gly	gta Val	ttt Phe 4175	Arg	gtt Val	caa Gln	aaa Lys	ttt Phe 4180	ggc Gly	cat His	13407
			Glu				tta Leu 4190	Asn	att Ile	gat Asp	aaa Lys	aca Thr 4195		ggt Gly	13452
		ata Ile 4200	Ser				aaa Lys 4205	Gln				ccc Pro 4210		cca Pro	13497
	_	gat Asp 4215	Leu				ttt Phe 4220	Leu				aat Asn 4225	Pro	tct Ser	13542
		act Thr 4230	Cys				gaa Glu 4235	Gly	aaa Lys	tat Tyr	ttg Leu	att Ile 4240	Asn	ggc Gly	13587
	_	aat Asn 4245	Asp	gac Asp	ago Ser	ctg Leu	tta Leu 4250	Asp				aag Lys 4255	Let	act Thr	13632

	_	gaa Glu	aat Asn 4260					att Ile 4265					ggt Gly 4270	-	ttg Leu	13677
		-	cac His 4275	_			_	tat Tyr 4280			_	_	tgt Cys 4285	_	gtc Val	13722
		cac His	tgt Cys 4290					cag Gln 4295					tgc Cys 4300	_	cca Pro	13767
		_						tgc Cys 4310					ggt Gly 4315		act Thr	13812
								gtc Val 4325			_		tgt Cys 4330	caa Gln	aat Asn	13857
How Girth		gga Gly						gct Ala 4340						tgc Cys		13902
Half first first has the first first the test test test.								gac Asp 4355					tac Tyr 4360	gtg Val	-	13947
			tat Tyr 4365					gaa Glu 4370					999 Gly 4375	gat Asp	_	13992
The field the first that the first the		agt Ser						cca Pro 4385					gga Gly 4390	cca Pro		14037
		gag Glu						agg Arg 4400					cac His 4405	tgc Cys	_	14082
								ata Ile 4415						aat Asn		14127
								tta Leu 4430						tac Tyr		14172
	ggt Gly	ggc Gly	aca Thr 4440	tgc Cys	cag Gln	ctg Leu	gac Asp	ccc Pro 4445	gag Glu	aca Thr	aat Asn	gta Val	cct Pro 4450	gtg Val	_	14217
	cta Leu	tgc Cys	tcc Ser 4455	acc Thr	aac Asn	tgg Trp	tca Ser	ggc Gly 4460	aca Thr	cag Gln	tgt Cys	gaa Glu	agg Arg 4465	cca Pro	gcc Ala	14262
			agc Ser 4470					cat His 4475					agc Ser 4480	att Ile	_	14307
								ttg Leu 4490						acc Thr		14352

the first that the that that the trail that the that the first that the

		ggt Gly 4500	tta Leu	gtg Val	ctt Leu	tgt Cys	aaa Lys 4505	aga Arg	aaa Lys	aga Arg	agg Arg	aca Thr 4510	aaa Lys		14397
att Ile	aga Arg	aga Arg 4515	caa Gln	cct Pro	att Ile	atc Ile	aat Asn 4520	gga Gly	gga Gly	ata Ile	aat Asn	gta Val 4525	gaa Glu		14442
ggc Gly	aat Asn	cca Pro 4530	tct Ser	tat Tyr	aac Asn	atg Met	tat Tyr 4535	gag Glu	gta Val	gat Asp	cat His	gat Asp 4540	cac His		14487
gat Asp	gga Gly	ggt Gly 4545	ctt Leu	tta Leu	gat Asp	cct Pro	ggc Gly 4550	ttt Phe	atg Met	ata Ile	gac Asp	cca Pro 4555	aca Thr	_	14532
_	agg Arg	tac Tyr 4560					ccc Pro 4565		gct Ala			ctt Leu 4570		cac His	14577
							aac Asn 4580					gga Gly 4585		cta Leu	14622
	_	999 Gly 4590					tcc Ser 4595		ccg Pro	gta Val	tat Tyr	gca Ala 4600	aaa Lys	tta Leu	14667
	_	gat Asp 4605	Gly				cga Arg 4610	Asn	tcc Ser	tta Leu	gga Gly	agt Ser 4615	gtt Val	gat Asp	14712
_		aaa Lys 4620	Ğlu				aag Lys 4625	Lys	ata Ile	gaa Glu	att Ile	ggt Gly 4630	ata Ile	aga Arg	14757
		gtg Val 4635	Āla		tcag	tga	tatct	ttta	t at	gctg	tata	aatg	tata	ag	14809
aat	atta	gga g	taca	tttg	g ta	tgtc	ccaa	cagg	tatt	at a	cgtg	gttgg	cat	cagcatt	14869
acc	tctt	tct t	tatc	tttt	t cc	tggt	taat	tgtt	ttct	ga g	tttt	ttggg	ttt	tatttt	14929
tgc	tgat	gac t	attg	attg	a cc	attt	gtat	ggta	tttt	ta t	gaaa	aagaa	ctg	cactaca	14989
gta	caat	tta c	aaca	atgc	t gc	tgat	atga	caca	cctt	tg a	attt	gttaa	aat	taaaaac	15049
aac	gtat	tcc t	ttgt	agtg	t ga	atat	gagc	aatc	tatt	tt a	tatg	aactt	ttt	tggttgt	15109
act	taat	caa c	gagg	agaa	t ct	ctgc	actt	ttcc	atta	ta c	ggtt	tgaag	gct	gtaatac	15169
agt	gtca	ttt t	attt	ttct	g tt	taaa	ttga	tgga	aaaa	tg a	ttga	atggt	caa	ctctctt	15229
ctt	tgtg	ccc a	ıtaaa	gato	g at	tcag	actc	tgct	gaaa	at a	tata	igctct	cac	aagttca	15289
gca	tcac	ctg c	ctttg	gaaat	t ag	cctt	agat	tgcc	aacc	aa t	agat	gagaa	ttt	tgaggaa	15349
aaa	aatt	aaa a	atat	gtaa	a at	taat	aatt	tgca	tgaa	ca c	agat	gacta	cat	tttccaa	15409
aac	ttag	tgg a	actct	atgt	g at	gtac	taaa	tgta	taca	icc t	tgta	agcaa	tag	ıttatatt	15469
tag	gtgg	tag a	acat	agca	a aa	atat	aacc	gaaa	gttg	igc c	gact	gcact	tgo	tatggaa:	15529

taagaccttt	tattctccct	cagtctcgag	ataaatagcc	agcctagagc	acaacagggc	15589
attgggtact	tgcatcttag	gtatttcttc	ccagtcacat	ccattttgtg	gaagattaac	15649
ccaacccctt	acactacact	gaacactaaa	gaataacata	taagcacaca	aattggtgac	15709
agaatttcaa	ttacgtgaac	gcatcctctt	tgctaggtca	aaaacaaagg	gcaaagcaga	15769
cattttagta	tacagagtga	ttggcaaata	ttttcaagat	ttaatatgag	caacccatta	15829
tttgccctat	ccaaaatata	ttcaagggcc	ttccaagttg	tagaagaaca	atgatcttcc	15889
cataatcaaa	agtggagagt	cgaaatgctg	tgccagttgc	tctggtattc	aggtttctct	15949
gggttttaca	gaacgcatgg	accccattca	cgtttggttt	gtttatcttc	aaatttgagt	16009
tgaaacgagt	gcgatttatt	taagttgtat	ataaaaataa	aaggatagca	tttttataca	16069
aatatcttta	aaggcacaaa	agatttattc	acaagttttg	gagggctttt	tgttcctctg	16129
atagacatga	ctgactttta	gctgtcataa	tgtattaacc	taacagatga	aatatgttaa	16189
atatgtggtt	gctctttatc	cctttgtaca	agcattaaaa	aaactgctgt	tttataagaa	16249
gactttttgt	tgtactatgt	gcatgcatac	tacctatttc	taaactttgc	catattgagg	16309
cctttataaa	ctattgattt	atgtaatact	agtgcaattt	tgcttgaaca	atgttatgca	16369
tatcataaac	tttttcaggt	tcttgtttaa	gtacattttt	taaattgaac	agtattttc	16429
attttggtta	taatatagtc	attttgccta	tgtttctaca	atgaagtgtt	aaatacttta	16489
taaaaaattg	ttgactgact	tatttaaatg	aaattctaca	tatttaaaaa	aaaaaa	16545

<210> 33

<211> 4636

<212> PRT

<213> Homo sapiens

<400> 33

Met Thr Pro Leu Gly Ser Arg Leu Gln Ala Ala Pro Ala Ala Ala Ala 1 5 10 15

Ala Ala Gly Pro Lys Val Pro Pro Ser Ser Leu Gln Arg Arg Leu Pro 20 25 30

Tyr Arg Ala Thr Thr Met Ser Glu Phe Leu Leu Ala Leu Leu Thr Leu 35 40 45

Ser Gly Leu Leu Pro Ile Ala Arg Val Leu Thr Val Gly Ala Asp Arg 50 55 60

Asp Gln Gln Leu Cys Asp Pro Gly Glu Phe Leu Cys His Asp His Val 65 70 75 80

Thr Cys Val Ser Arg Ser Trp Leu Cys Asp Gly Asp Pro Asp Cys Pro

Asp	Asp	Ser	100	Glu	Ser	Leu	Asp	Thr 105	Cys	Pro	GIu	Glu	110	GIU	116
Lys	Cys	Pro 115	Leu	Asn	His	Ile	Ala 120	Cys	Leu	Gly	Thr	Asn 125	Lys	Cys	Val
His	Leu 130	Ser	Gln	Leu	Cys	Asn 135	Gly	Val	Leu	Asp	Cys 140	Pro	Asp	Gly	Tyr
Asp 145	Glu	Gly	Val	His	Cys 150	Gln	Glu	Leu	Leu	Ser 155	Asn	Cys	Gln	Gln	Leu 160
Asn	Cys	Gln	Tyr	Lys 165	Cys	Thr	Met	Val	Arg 170	Asn	Ser	Thr	Arg	Cys 175	Tyr
Cys	Glu	Asp	Gly 180	Phe	Glu	Ile	Thr	Glu 185	Asp	Gly	Arg	Ser	Cys 190	Lys	Asp
Gln	Asp	Glu 195	Cys	Ala	Val	туг	Gly 200	Thr	Cys	Ser	Gln	Thr 205	Cys	Arg	Asn
Thr	His 210	Gly	Ser	Tyr	Thr	Cys 215	Ser	Cys	Val	Glu	Gly 220	Tyr	Leu	Met	Gln
Pro 225	Asp	Asn	Arg	Ser	Cys 230	Lys	Ala	Lys	Ile	Glu 235	Pro	Thr	Asp	Arg	Pro 240
Pro	Ile	Leu	Leu	Ile 245	Ala	Asn	Phe	Glu	Thr 250	Ile	Glu	Val	Phe	Tyr 255	Leu
Asn	Gly	Ser	Lys 260	Met	Ala	Thr	Leu	Ser 265	Ser	Val	Asn	Gly	Asn 270	Glu	Ile
His	Thr	Leu 275		Phe	Ile	Tyr	Asn 280	Glu	Asp	Val	Ile	Cys 285	Trp	Ile	Glu
Ser	Arg 290		Ser	Ser	Asn	Gln 295		Lys	Cys	Ile	Gln 300		Thr	Lys	Ala
Gly 305		Leu	Thr	Asp	Glu 310		Thr	Ile	Asn	Ile 315		Gln	Ser	Phe	His 320
Asn	Val	Gln	Gln	. Met 325	Ala	Ile	Asp	Trp	Leu 330		Arg	Asn	Leu	Tyr 335	Phe

Val Asp His Val Gly Asp Arg Ile Phe Val Cys Asn Ser Asn Gly Ser 340 345 350

Val Cys Val Thr Leu Ile Asp Leu Glu Leu His Asn Pro Lys Ala Ile 355 360 365

Ala Val Asp Pro Ile Ala Gly Lys Leu Phe Phe Thr Asp Tyr Gly Asn 370 380

Val Ala Lys Val Glu Arg Cys Asp Met Asp Gly Met Asn Arg Thr Arg 385 390 395 400

Ile Ile Asp Ser Lys Thr Glu Gln Pro Ala Ala Leu Ala Leu Asp Leu 405 410 415

Val Asn Lys Leu Val Tyr Trp Val Asp Leu Tyr Leu Asp Tyr Val Gly 420 425 430

Val Val Asp Tyr Gln Gly Lys Asn Arg His Thr Val Ile Gln Gly Arg 435 440 445

Gln Val Arg His Leu Tyr Gly Ile Thr Val Phe Glu Asp Tyr Leu Tyr 450 455 460

Ala Thr Asn Ser Asp Asn Tyr Asn Ile Val Arg Ile Asn Arg Phe Asn 465 470 475 480

Gly Thr Asp Ile His Ser Leu Ile Lys Ile Glu Asn Ala Trp Gly Ile 485 490 495

Arg Ile Tyr Gln Lys Arg Thr Gln Pro Thr Val Arg Ser His Ala Cys 500 505 510

Glu Val Asp Pro Tyr Gly Met Pro Gly Gly Cys Ser His Ile Cys Leu 515 520 525

Leu Ser Ser Ser Tyr Lys Thr Arg Thr Cys Arg Cys Arg Thr Gly Phe 530 535 540

Asn Leu Gly Ser Asp Gly Arg Ser Cys Lys Arg Pro Lys Asn Glu Leu 545 550 555 560

Phe Leu Phe Tyr Gly Lys Gly Arg Pro Gly Ile Val Arg Gly Met Asp 565 570 575

Leu Asn Thr Lys Ile Ala Asp Glu Tyr Met Ile Pro Ile Glu Asn Leu 580 585 590

Val Asn Pro Arg Ala Leu Asp Phe His Ala Glu Thr Asn Tyr Ile Tyr 595 600 605

Phe Ala Asp Thr Thr Ser Phe Leu Ile Gly Arg Gln Lys Ile Asp Gly 610 615 620

Thr Glu Arg Glu Thr Ile Leu Lys Asp Asp Leu Asp Asn Val Glu Gly 625 630 635 640

Ile Ala Val Asp Trp Ile Gly Asn Asn Leu Tyr Trp Thr Asn Asp Gly 645 650 655

His Arg Lys Thr Ile Asn Val Ala Arg Leu Glu Lys Ala Ser Gln Ser 660 665 670

Arg Lys Thr Leu Leu Glu Gly Glu Met Ser His Pro Arg Gly Ile Val 675 680 685

Val Asp Pro Ile Asn Gly Trp Met Tyr Trp Thr Asp Trp Glu Glu Asp 690 695 700

Glu Ile Asp Asp Ser Val Gly Arg Ile Glu Lys Ala Trp Met Asp Gly 705 710 715 715 720

Phe Asn Arg Gln Ile Phe Val Thr Ser Lys Met Leu Trp Pro Asn Gly 725 730 735

Leu Thr Leu Asp Phe His Thr Asn Thr Leu Tyr Trp Cys Asp Ala Tyr 740 745 750

Tyr Asp His Ile Glu Lys Val Phe Leu Asn Gly Thr His Arg Lys Ile 755 760 765

Val Tyr Ser Gly Arg Glu Leu Asn His Pro Phe Gly Leu Ser His His 770 780

Gly Asn Tyr Val Phe Trp Thr Asp Tyr Met Asn Gly Ser Ile Phe Gln 785 790 795 800

Leu Asp Leu Ile Thr Ser Glu Val Thr Leu Leu Arg His Glu Arg Pro 805 810 815

Pro Leu Phe Gly Leu Gln Ile Tyr Asp Pro Arg Lys Gln Gln Gly Asp 820 825 830

Asn Met Cys Arg Val Asn Asn Gly Gly Cys Ser Thr Leu Cys Leu Ala 835 840 845

- Ile Pro Gly Gly Arg Val Cys Ala Cys Ala Asp Asn Gln Leu Leu Asp 850 860
- Glu Asn Gly Thr Thr Cys Thr Phe Asn Pro Gly Glu Ala Leu Pro His 865 870 875 880
- Ile Cys Lys Ala Gly Glu Phe Arg Cys Lys Asn Arg His Cys Ile Gln 885 890 895
- Ala Arg Trp Lys Cys Asp Gly Asp Asp Asp Cys Leu Asp Gly Ser Asp 900 905 910
- Glu Asp Ser Val Asn Cys Phe Asn His Ser Cys Pro Asp Asp Gln Phe 915 920 925
- Lys Cys Gln Asn Asn Arg Cys Ile Pro Lys Arg Trp Leu Cys Asp Gly 930 935 940
- Ala Asn Asp Cys Gly Ser Asn Glu Asp Glu Ser Asn Gln Thr Cys Thr 945 950 955 960
- Ala Arg Thr Cys Gln Val Asp Gln Phe Ser Cys Gly Asn Gly Arg Cys 965 970 975
- Ile Pro Arg Ala Trp Leu Cys Asp Arg Glu Asp Asp Cys Gly Asp Gln 980 985 990
- Thr Asp Glu Met Ala Ser Cys Glu Phe Pro Thr Cys Glu Pro Leu Thr 995 1000 1005
- Gln Phe Val Cys Lys Ser Gly Arg Cys Ile Ser Ser Lys Trp His 1010 1015 1020
- Cys Asp Ser Asp Asp Asp Cys Gly Asp Gly Ser Asp Glu Val Gly 1025 1030 1035
- Cys Val His Ser Cys Phe Asp Asn Gln Phe Arg Cys Ser Ser Gly 1040 1045 1050
- Arg Cys Ile Pro Gly His Trp Ala Cys Asp Gly Asp Asn Asp Cys 1055 1060 1065
- Gly Asp Phe Ser Asp Glu Ala Gln Ile Asn Cys Thr Lys Glu Glu 1070 1075 1080
- Ile His Ser Pro Ala Gly Cys Asn Gly Asn Glu Phe Gln Cys His 1085 1090 1095

Pro Asp Gly Asn Cys Val Pro Asp Leu Trp Arg Cys Asp Gly Glu 1105 1110 1100 Lys Asp Cys Glu Asp Gly Ser Asp Glu Lys Gly Cys Asn Gly Thr 1120 1115 Ile Arg Leu Cys Asp His Lys Thr Lys Phe Ser Cys Trp Ser Thr 1135 Gly Arg Cys Ile Asn Lys Ala Trp Val Cys Asp Gly Asp Ile Asp 1155 1150 Cys Glu Asp Gln Ser Asp Glu Asp Asp Cys Asp Ser Phe Leu Cys 1165 Gly Pro Pro Lys His Pro Cys Ala Asn Asp Thr Ser Val Cys Leu 1175 1180 1185 Gln Pro Glu Lys Leu Cys Asn Gly Lys Lys Asp Cys Pro Asp Gly 1200 1195 1190 Ser Asp Glu Gly Tyr Leu Cys Asp Glu Cys Ser Leu Asn Asn Gly 1215 1210 1205 Gly Cys Ser Asn His Cys Ser Val Val Pro Gly Arg Gly Ile Val 1225 1220 Cys Ser Cys Pro Glu Gly Leu Gln Leu Asn Lys Asp Asn Lys Thr 1240 1235 Cys Glu Ile Val Asp Tyr Cys Ser Asn His Leu Lys Cys Ser Gln 1255 1250 Val Cys Glu Gln His Lys His Thr Val Lys Cys Ser Cys Tyr Glu 1270 1265 Gly Trp Lys Leu Asp Val Asp Gly Glu Ser Cys Thr Ser Val Asp 1285 1290 Pro Phe Glu Ala Phe Ile Ile Phe Ser Ile Arg His Glu Ile Arg 1300 1295 Arg Ile Asp Leu His Lys Arg Asp Tyr Ser Leu Leu Val Pro Gly 1320 1315 1310 Leu Arg Asn Thr Ile Ala Leu Asp Phe His Phe Asn Gln Ser Leu 1330 1325

- Leu Tyr Trp Thr Asp Val Val Glu Asp Arg Ile Tyr Arg Gly Lys 1340 1345 1350
- Leu Ser Glu Ser Gly Gly Val Ser Ala Ile Glu Val Val Glu 1355 1360 1365
- His Gly Leu Ala Thr Pro Glu Gly Leu Thr Val Asp Trp Ile Ala 1370 1375 1380
- Gly Asn Ile Tyr Trp Ile Asp Ser Asn Leu Asp Gln Ile Glu Val 1385 1390 1395
- Ala Lys Leu Asp Gly Ser Leu Arg Thr Thr Leu Ile Ala Gly Ala 1400 1410
- Met Glu His Pro Arg Ala Ile Ala Leu Asp Pro Arg Tyr Gly Ile 1415 1420 1425
- Leu Phe Trp Thr Asp Trp Asp Ala Asn Phe Pro Arg Ile Glu Ser 1430 1435
- Ala Ser Met Ser Gly Ala Gly Arg Lys Thr Ile Tyr Lys Asp Met 1445 1450 1455
- Lys Thr Gly Ala Trp Pro Asn Gly Leu Thr Val Asp His Phe Glu 1460 1465 1470
- Lys Arg Ile Val Trp Thr Asp Ala Arg Ser Asp Ala Ile Tyr Ser 1475 1480 1485
- Ala Leu Tyr Asp Gly Thr Asn Met Ile Glu Ile Ile Arg Gly His 1490 1495 1500
- Glu Tyr Leu Ser His Pro Phe Ala Val Ser Leu Tyr Gly Ser Glu 1505 1510 1515
- Val Tyr Trp Thr Asp Trp Arg Thr Asn Thr Leu Ser Lys Ala Asn 1520 1530
- Lys Trp Thr Gly Gln Asn Val Ser Val Ile Gln Lys Thr Ser Ala 1535 1540 1545
- Gln Pro Phe Asp Leu Gln Ile Tyr His Pro Ser Arg Gln Pro Gln 1550 1555 1560
- Ala Pro Asn Pro Cys Ala Ala Asn Asp Gly Lys Gly Pro Cys Ser 1565 1570 1575

- His Met Cys Leu Ile Asn His Asn Arg Ser Ala Ala Cys Ala Cys 1580 1585 1590
- Pro His Leu Met Lys Leu Ser Ser Asp Lys Lys Thr Cys Tyr Glu 1595 1600 1605
- Met Lys Lys Phe Leu Leu Tyr Ala Arg Arg Ser Glu Ile Arg Gly 1610 1615 1620
- Val Asp Ile Asp Asn Pro Tyr Phe Asn Phe Ile Thr Ala Phe Thr 1625 1630 1635
- Val Pro Asp Ile Asp Asp Val Thr Val Ile Asp Phe Asp Ala Ser 1640 1645 1650
- Glu Glu Arg Leu Tyr Trp Thr Asp Ile Lys Thr Gln Thr Ile Lys 1655 1660 1665
- Arg Ala Phe Ile Asn Gly Thr Gly Leu Glu Thr Val Ile Ser Arg 1670 1680
- Asp Ile Gln Ser Ile Arg Gly Leu Ala Val Asp Trp Val Ser Arg 1685 1690 1695
- Asn Leu Tyr Trp Ile Ser Ser Glu Phe Asp Glu Thr Gln Ile Asn 1700 1705 1710
- Val Ala Arg Leu Asp Gly Ser Leu Lys Thr Ser Ile Ile His Gly 1715 1720 1725
- Ile Asp Lys Pro Gln Cys Leu Ala Ala His Pro Val Arg Gly Lys 1730 1740
- Leu Tyr Trp Thr Asp Gly Asn Thr Ile Asn Met Ala Asn Met Asp 1745 1750 1755
- Gly Ser Asn Ser Lys Ile Leu Phe Gln Asn Gln Lys Glu Pro Val 1760 1765 1770
- Gly Leu Ser Ile Asp Tyr Val Glu Asn Lys Leu Tyr Trp Ile Ser 1775 1780 1785
- Ser Gly Asn Gly Thr Ile Asn Arg Cys Asn Leu Asp Gly Gly Asn 1790 1795 1800
- Leu Glu Val Ile Glu Ser Met Lys Glu Glu Leu Thr Lys Ala Thr 1805 1810 1815

Ala Leu Thr Ile Met Asp Lys Lys Leu Trp Trp Ala Asp Gln Asn 1820 1825 1830

Leu Ala Gln Leu Gly Thr Cys Ser Lys Arg Asp Gly Arg Asn Pro 1835 1840 1845

Thr Ile Leu Arg Asn Lys Thr Ser Gly Val Val His Met Lys Val 1850 1855 1860

Tyr Asp Lys Glu Ala Gln Gln Gly Ser Asn Ser Cys Gln Leu Asn 1865 1870 1875

Asn Gly Gly Cys Ser Gln Leu Cys Leu Pro Thr Ser Glu Thr Thr 1880 1885 1890

Arg Thr Cys Met Cys Thr Val Gly Tyr Tyr Leu Gln Lys Asn Arg 1895 1900 1905

Met Ser Cys Gln Gly Ile Glu Ser Phe Leu Met Tyr Ser Val His 1910 1915 1920

Glu Gly Ile Arg Gly Ile Pro Leu Glu Pro Ser Asp Lys Met Asp 1925 1930 1935

Ala Leu Met Pro Ile Ser Gly Thr Ser Phe Ala Val Gly Ile Asp 1940 1945 1950

Phe His Ala Glu Asn Asp Thr Ile Tyr Trp Thr Asp Met Gly Phe 1955 1960 1965

Asn Lys Ile Ser Arg Ala Lys Arg Asp Gln Thr Trp Lys Glu Asp 1970 1975 1980

Ile Ile Thr Asn Gly Leu Gly Arg Val Glu Gly Ile Ala Val Asp 1985 1990 1995

Trp Ile Ala Gly Asn Ile Tyr Trp Thr Asp His Gly Phe Asn Leu 2000 2005 2010

Ile Glu Val Ala Arg Leu Asn Gly Ser Phe Arg Tyr Val Ile Ile 2015 2020 2025

Ser Gln Gly Leu Asp Gln Pro Arg Ser Ile Ala Val His Pro Glu 2030 2035 2040

Lys Gly Leu Leu Phe Trp Thr Glu Trp Gly Gln Met Pro Cys Ile 2045 2050 2055

Gly	Lys 2060	Ala	Arg	Leu	Asp	Gly 2065	Ser	Glu	Lys	Val	Val 2070	Leu	Val	Ser

Met Gly Ile Ala Trp Pro Asn Gly Ile Ser Ile Asp Tyr Glu Glu 2075 2080 2085

Asn Lys Leu Tyr Trp Cys Asp Ala Arg Thr Asp Lys Ile Glu Arg 2090 2095 2100

Ile Asp Leu Glu Thr Gly Gly Asn Arg Glu Met Val Leu Ser Gly 2105 2110 2115

Ser Asn Val Asp Met Phe Ser Val Ala Val Phe Gly Ala Tyr Ile 2120 2130

Tyr Trp Ser Asp Arg Ala His Ala Asn Gly Ser Val Arg Arg Gly 2135 2140 2145

His Lys Asn Asp Ala Thr Glu Thr Ile Thr Met Arg Thr Gly Leu 2150 2160

Gly Val Asn Leu Lys Glu Val Lys Ile Phe Asn Arg Val Arg Glu 2165 2170 2175

Lys Gly Thr Asn Val Cys Ala Arg Asp Asn Gly Gly Cys Lys Gln 2180 2185 2190

Leu Cys Leu Tyr Arg Gly Asn Ser Arg Arg Thr Cys Ala Cys Ala 2195 2200 2205

His Gly Tyr Leu Ala Glu Asp Gly Val Thr Cys Leu Arg His Glu 2210 2215 2220

Gly Tyr Leu Leu Tyr Ser Gly Arg Thr Ile Leu Lys Ser Ile His 2225 2230 2235

Leu Ser Asp Glu Thr Asn Leu Asn Ser Pro Ile Arg Pro Tyr Glu 2240 2245 2250

Asn Pro Arg Tyr Phe Lys Asn Val Ile Ala Leu Ala Phe Asp Tyr 2255 2260 2265

Asn Gln Arg Arg Lys Gly Thr Asn Arg Ile Phe Tyr Ser Asp Ala 2270 2275 2280

His Phe Gly Asn Ile Gln Leu Ile Lys Asp Asn Trp Glu Asp Arg 2285 2290 2295

- Gln Val Ile Val Glu Asn Val Gly Ser Val Glu Gly Leu Ala Tyr 2300 2305 2310
- His Arg Ala Trp Asp Thr Leu Tyr Trp Thr Ser Ser Thr Thr Ser 2315 2320 2325
- Ser Ile Thr Arg His Thr Val Asp Gln Thr Arg Pro Gly Ala Phe 2330 2340
- Asp Arg Glu Ala Val Ile Thr Met Ser Glu Asp Asp His Pro His 2345 2350 2355
- Val Leu Ala Leu Asp Glu Cys Gln Asn Leu Met Phe Trp Thr Asn 2360 2370
- Trp Asn Glu Gln His Pro Ser Ile Met Arg Ser Thr Leu Thr Gly 2375 2380 2385
- Lys Asn Ala Gln Val Val Ser Thr Asp Ile Leu Thr Pro Asn 2390 2395 2400
- Gly Leu Thr Ile Asp Tyr Arg Ala Glu Lys Leu Tyr Phe Ser Asp 2405 2410 2415
- Gly Ser Leu Gly Lys Ile Glu Arg Cys Glu Tyr Asp Gly Ser Gln 2420 2425 2430
- Arg His Val Ile Val Lys Ser Gly Pro Gly Thr Phe Leu Ser Leu 2435 2440 2445
- Ala Val Tyr Asp Asn Tyr Ile Phe Trp Ser Asp Trp Gly Arg Arg 2450 2455 2460
- Ala Ile Leu Arg Ser Asn Lys Tyr Thr Gly Gly Asp Thr Lys Ile 2465 2470 2475
- Leu Arg Ser Asp Ile Pro His Gln Pro Met Gly Ile Ile Ala Val 2480 2485 2490
- Ala Asn Asp Thr Asn Ser Cys Glu Leu Ser Pro Cys Ala Leu Leu 2495 2500 2505
- Asn Gly Gly Cys His Asp Leu Cys Leu Leu Thr Pro Asn Gly Arg 2510 2515 2520
- Val Asn Cys Ser Cys Arg Gly Asp Arg Ile Leu Leu Glu Asp Asn 2525 2530 2535

-	Cys 2540	Val	Thr	Lys	Asn	Ser 2545	Ser	Cys	Asn	Ala	Tyr 2550	Ser	Glu	Phe
	Cys 2555	Gly	Asn	Gly	Glu	Cys 2560	Ile	Asp	Tyr	Gln	Leu 2565	Thr	Cys	Asp
	Ile 2570	Pro	His	Cys	Lys	Asp 2575	Lys	Ser	Asp	Glu	Lys 2580	Leu	Leu	Tyr
-	Glu 2585	Asn	Arg	Ser	Cys	Arg 2590	Arg	Gly	Phe		Pro 2595	Cys	Tyr	Asn
	Arg 2600		Ile	Pro	His	Gly 2605	Lys	Leu	Cys	Asp	Gly 2610	Glu	Asn	Asp
_	Gly 2615		Asn	Ser	Asp	Glu 2620	Leu	Asp	Cys	Lys	Val 2625	Ser	Thr	Cys
Ala	Thr 2630		Glu	Phe	Arg	Cys 2635		Asp	Gly	Thr	Cys 2640	Ile	Pro	Arg
Ser	Ala 2645		Cys	Asn	Gln	Asn 2650	Ile	Asp	Cys	Ala	Asp 2655	Ala	Ser	Asp
	Lys 2660		Cys	Asn	Asn	Thr 2665		Cys	Thr	His	Phe 2670	Tyr	Lys	Leu
Gly	Val 2675		Thr	Thr		Phe 2680		Arg	Cys	Asn	Ser 2685	Thr	Ser	Leu
Cys	Val 2690		Pro	Thr	Trp	Ile 2695		Asp	Gly	Ser	Asn 2700	Asp	Cys	Gly
Asp	Tyr 2705		Asp	Glu	Leu	Lys 2710		Pro	Val	Gln	Asn 2715	Lys	His	Lys
Cys	Glu 2720		Asn	Tyr	Phe	Ser 2725		Pro	Ser	Gly	Arg 2730	Cys	Ile	Leu
Asn	Thr 2735		Ile	Cys	Asp	Gly 2740		Lys	Asp	Сув	Glu 2745	Asp	Gly	Arg
Asp	Glu 2750		His	Cys	Asp	Ser 2755		Cys	Ser	Trp	Asn 2760		n Phe	Ala
Cys	Ser 2765		Glr	ı Lys	Cys	1le 2770		Lys	His	Trp	1le 2775		a Asp	Gly

	Asp 2780	Asp	Cys	Gly	Asp	Gly 2785	Leu	Asp	Glu	Ser	Asp 2790	Ser	Ile	Cys
-	Ala 2795	Ile	Thr	Cys	Ala	Ala 2800	Asp	Met	Phe	Ser	Cys 2805	Gln	Gly	Ser
	Ala 2810	Cys	Val	Pro	Arg	His 2815	Trp	Leu	Cys	Asp	Gly 2820	Glu	Arg	Asp
	Pro 2825		Gly	Ser	Asp	Glu 2830	Leu	Ser	Thr	Ala	Gly 2835	Cys	Ala	Pro
Asn	Asn 2840	Thr	Cys	Asp	Glu	Asn 2845	Ala	Phe	Met	Cys	His 2850	Asn	Lys	Val
Cys	Ile 2855		Lys	Gln	Phe	Val 2860		Asp	His	Asp	Asp 2865	Asp	Cys	Gly
Asp	Gly 2870		Asp	Glu	Ser	Pro 2875		Cys	Gly	Tyr	Arg 2880	Gln	Cys	Gly
Thr	Glu 2885		Phe	Ser	Cys	Ala 2890	Asp	Gly	Arg	Cys	Leu 2895	Leu	Asn	Thr
Gln	Trp 2900		Cys	Asp		Asp 2905		Asp	Cys	Pro	Asp 2910	His	Ser	Asp
Glu	Ala 2915		Leu	Asn	Pro	Lys 2920		Lys	Ser	Ala	Glu 2925	Gln	Ser	Cys
Asn	Ser 2930		Phe	Phe	Met	Сув 2935		Asn	Gly	Arg	Cys 2940	Ile	Pro	Ser
Gly	Gly 2945		Cys	Asp	Asn	. Lys 2950		Asp	Cys	Gly	Asp 2955	Gly	Ser	Asp
Glu	Arg 2960		Cys	. His	Ile	: Asn 2965		Cys	Leu	Ser	Lys' 2970	Lys	Val	Ser
Gly	Cys 2975		Glr	ı Asp	Cys	Gln 2980		Leu	Pro	Val	Ser 2985	Tyr	. Lys	Cys
Lys	Cys 2990		Pro	Gly	⁄ Ph∈	e Gln 2995		Lys	Asp	Asp	Gly 3000	Lys	. Thr	Cys
Val	Asp 3005		e Asp	o Glu	ı Cys	s Ser 3010		Gly	Phe	Pro	Cys 3015	Ser	Glr	ı Gln

Cys	Ile 3020		Thr	Tyr	Gly	Thr 3025	Tyr	Lys	Cys	Leu	Cys 3030	Thr	Asp	Gly
Tyr	Glu 3035		Gln	Pro	-	Asn 3040	Pro	Asn	Gly	Cys	Lys 3045	Ser	Leu	Ser
Asp	Glu 3050	Glu	Pro	Phe	Leu	Ile 3055	Leu	Ala	Asp	His	His 3060	Glu	Ile	Arg
Lys	Ile 3065	Ser	Thr	Asp	Gly	Ser 3070	Asn	Tyr	Thr	Leu	Leu 3075	Lys	Gln	Gly
Leu	Asn 3080		Val	Ile	Ala	Ile 3085		Phe	Asp	Tyr	Arg 3090	Glu	Glu	Phe
Ile	Tyr 3095	Trp	Ile	Asp	Ser	Ser 3100	Arg	Pro	Asn	Gly	Ser 3105	Arg	Ile	Asn
Arg	Met 3110		Leu	Asn	Gly	Ser 3115	Asp	Ile	Lys	Val	Val 3120	His	Asn	Thr
Ala	Val 3125		Asn	Ala		Ala 3130	Val	Asp	Trp	Ile	Gly 3135	Lys	Asn	Leu
Tyr	Trp 3140	Ser	Asp	Thr	Glu	Lys 3145	Arg	Ile	Ile	Glu.	Val 3150	Ser	Lys	Leu
Asn	Gly 3155		Tyr	Pro	Thr	Ile 3160	Leu	Val	Ser	Lys	Arg 3165	Leu	Lys	Phe
Pro	Arg 3170		Leu	Ser		Asp 3175	Pro	Gln	Ala	Gly	Tyr 3180	Leu	Tyr	Trp
Ile	Asp 3185	Cys	Cys	Glu	Tyr	Pro 3190	His	Ile	Gly	Arg	Val 3195	Gly	Met	Ąsp
Gly	Thr 3200	Asn	Gln	Ser	Val	Val 3205	Ile	Glu	Thr	Lys	Ile 3210	Ser	Arg	Pro
Met	Ala 3215	Leu	Thr	Ile	Asp	Tyr 3220	Val	Asn	Arg	Arg	Leu 3225	Tyr	Trp	Ala
Asp	Glu 3230	Asn	His	Ile	Glu	Phe 3235	Ser	Asn	Met	Asp	Gly 3240	Ser	His	Arg
His	Lys 3245	Val	Pro	Asn	Gln	Asp 3250	Ile	Pro	Gly	Val	Ile 3255	Ala	Leu	Thr

Leu Phe Glu Asp Tyr Ile Tyr Trp Thr Asp Gly Lys Thr Lys Ser 3260 3265 3270

Leu Ser Arg Ala His Lys Thr Ser Gly Ala Asp Arg Leu Ser Leu 3275 3280 3285

Ile Tyr Ser Trp His Ala Ile Thr Asp Ile Gln Val Tyr His Ser 3290 3295 3300

Tyr Arg Gln Pro Asp Val Ser Lys His Leu Cys Met Ile Asn Asn 3305 3310 3315

Gly Gly Cys Ser His Leu Cys Leu Leu Ala Pro Gly Lys Thr His 3320 3330

Thr Cys Ala Cys Pro Thr Asn Phe Tyr Leu Ala Ala Asp Asn Arg 3335 3340 3345

Thr Cys Leu Ser Asn Cys Thr Ala Ser Gln Phe Arg Cys Lys Thr 3350 3355 3360

Asp Lys Cys Ile Pro Phe Trp Trp Lys Cys Asp Thr Val Asp Asp 3365 3370 3375

Cys Gly Asp Gly Ser Asp Glu Pro Asp Asp Cys Pro Glu Phe Arg 3380 3385 3390

Cys Gln Pro Gly Arg Phe Gln Cys Gly Thr Gly Leu Cys Ala Leu 3395 3400 3405

Pro Ala Phe Ile Cys Asp Gly Glu Asn Asp Cys Gly Asp Asn Ser 3410 3420

Asp Glu Leu Asn Cys Asp Thr His Val Cys Leu Ser Gly Gln Phe 3425 3430 3435

Lys Cys Thr Lys Asn Gln Lys Cys Ile Pro Val Asn Leu Arg Cys 3440 3445 3450

Asn Gly Gln Asp Asp Cys Gly Asp Glu Glu Asp Glu Arg Asp Cys 3455 3460 3465

Pro Glu Asn Ser Cys Ser Pro Asp Tyr Phe Gln Cys Lys Thr Thr 3470 3475 3480

Lys His Cys Ile Ser Lys Leu Trp Val Cys Asp Glu Asp Pro Asp 3485 3490 3495

- Cys Ala Asp Ala Ser Asp Glu Ala Asn Cys Asp Lys Lys Thr Cys 3500 3510
- Gly Pro His Glu Phe Gln Cys Lys Asn Asn Asn Cys Ile Pro Asp 3515 3520 3525
- His Trp Arg Cys Asp Ser Gln Asn Asp Cys Ser Asp Asn Ser Asp 3530 3540
- Glu Glu Asn Cys Lys Pro Gln Thr Cys Thr Leu Lys Asp Phe Leu 3545 3550 3555
- Cys Ala Asn Gly Asp Cys Val Ser Ser Arg Phe Trp Cys Asp Gly 3560 3565 3570
- Asp Phe Asp Cys Ala Asp Gly Ser Asp Glu Arg Asn Cys Glu Thr 3575 3580 3585
- Ser Cys Ser Lys Asp Gln Phe Arg Cys Ser Asn Gly Gln Cys Ile 3590 3595 3600
- Pro Ala Lys Trp Lys Cys Asp Gly His Glu Asp Cys Lys Tyr Gly 3605 3610 3615
- Glu Asp Glu Lys Ser Cys Glu Pro Ala Ser Pro Thr Cys Ser Ser 3620 3630
- Arg Glu Tyr Ile Cys Ala Ser Asp Gly Cys Ile Ser Ala Ser Leu 3635 3640 3645
- Lys Cys Asn Gly Glu Tyr Asp Cys Ala Asp Gly Ser Asp Glu Met 3650 3660
- Asp Cys Val Thr Glu Cys Lys Glu Asp Gln Phe Arg Cys Lys Asn 3665 3670 3675
- Lys Ala His Cys Ile Pro Ile Arg Trp Leu Cys Asp Gly Ile His 3680 3685 3690
- Asp Cys Val Asp Gly Ser Asp Glu Glu Asn Cys Glu Arg Gly Gly 3695 3700 3705
- Asn Ile Cys Arg Ala Asp Glu Phe Leu Cys Asn Asn Ser Leu Cys 3710 3720
- Lys Leu His Phe Trp Val Cys Asp Gly Glu Asp Asp Cys Gly Asp 3725 3730 3735

Asn	Ser	Asp	Glu	Ala	Pro	Asp	Met	Cys	Val	Lys	Phe	Leu	Cys	Pro
	3740					3745					3750			

- Ser Thr Arg Pro His Arg Cys Arg Asn Asn Arg Ile Cys Leu Gln 3755 3760 3765
- Ser Glu Gln Met Cys Asn Gly Ile Asp Glu Cys Gly Asp Asn Ser 3770 3775 3780
- Asp Glu Asp His Cys Gly Gly Lys Leu Thr Tyr Lys Ala Arg Pro 3785 3790 3795
- Cys Lys Lys Asp Glu Phe Ala Cys Ser Asn Lys Lys Cys Ile Pro
- Met Asp Leu Gln Cys Asp Arg Leu Asp Asp Cys Gly Asp Gly Ser 3815 3820 3825
- Asp Glu Gln Gly Cys Arg Ile Ala Pro Thr Glu Tyr Thr Cys Glu 3830 3840
- Asp Asn Val Asn Pro Cys Gly Asp Asp Ala Tyr Cys Asn Gln Ile 3845 3850 3855
- Lys Thr Ser Val Phe Cys Arg Cys Lys Pro Gly Phe Gln Arg Asn 3860 3865 3870
- Met Lys Asn Arg Gln Cys Glu Asp Leu Asn Glu Cys Leu Val Phe 3875 3880 3885
- Gly Thr Cys Ser His Gln Cys Ile Asn Val Glu Gly Ser Tyr Lys 3890 3895 3900
- Cys Val Cys Asp Gln Asn Phe Gln Glu Arg Asn Asn Thr Cys Ile 3905 3910 3915
- Ala Glu Gly Ser Glu Asp Gln Val Leu Tyr Ile Ala Asn Asp Thr 3920 3925 3930
- Asp Ile Leu Gly Phe Ile Tyr Pro Phe Asn Tyr Ser Gly Asp His 3935 3940 3945
- Gln Gln Ile Ser His Ile Glu His Asn Ser Arg Ile Thr Gly Met 3950 3960
- Asp Val Tyr Tyr Gln Arg Asp Met Ile Ile Trp Ser Thr Gln Phe 3965 3970 3975

Asn Pro Gly Gly Ile Phe Tyr Lys Arg Ile His Gly Arg Glu Lys 3980 3985 3990

Arg Gln Ala Asn Ser Gly Leu Ile Cys Pro Glu Phe Lys Arg Pro

Arg Asp Ile Ala Val Asp Trp Val Ala Gly Asn Ile Tyr Trp Thr 4010 4015 4020

Asp His Ser Arg Met His Trp Phe Ser Tyr Tyr Thr Thr His Trp 4025 4030 4035

Thr Ser Leu Arg Tyr Ser Ile Asn Val Gly Gln Leu Asn Gly Pro 4040 4045 4050

Asn Cys Thr Arg Leu Leu Thr Asn Met Ala Gly Glu Pro Tyr Ala 4055 4060 4065

Ile Ala Val Asn Pro Lys Arg Gly Met Met Tyr Trp Thr Val Val 4070 4075 4080

Gly Asp His Ser His Ile Glu Glu Ala Ala Met Asp Gly Thr Leu 4085 4090 4095

Arg Arg Ile Leu Val Gln Lys Asn Leu Gln Arg Pro Thr Gly Leu 4100 4105 4110

Ala Val Asp Tyr Phe Ser Glu Arg Ile Tyr Trp Ala Asp Phe Glu 4115 4120 4125

Leu Ser Ile Ile Gly Ser Val Leu Tyr Asp Gly Ser Asn Ser Val 4130 4135 4140

Val Ser Val Ser Ser Lys Gln Gly Leu Leu His Pro His Arg Ile 4145 4150 4155

Asp Ile Phe Glu Asp Tyr Ile Tyr Gly Ala Gly Pro Lys Asn Gly 4160 4165 4170

Val Phe Arg Val Gln Lys Phe Gly His Gly Ser Val Glu Tyr Leu 4175 4180 4185

Ala Leu ·Asn Ile Asp Lys Thr Lys Gly Val Leu Ile Ser His Arg 4190 4195 4200

Tyr Lys Gln Leu Asp Leu Pro Asn Pro Cys Leu Asp Leu Ala Cys 4205 4210 4215

Glu	Phe 4220	Leu	Cys	Leu	Leu	Asn 4225		Ser	Gly	Ala	Thr 4230	Cys	Val	Cys
Pro	Glu 4235	Gly	Lys	Tyr	Leu	Ile 4240	Asn	Gly	Thr	Cys	Asn 4245	Asp	Asp	Ser
Leu	Leu 4250	Asp	Asp	Ser	Cys	Lys 4255	Leu	Thr	Cys	Glu	Asn 4260	Gly	Gly	Arg
Cys	Ile 4265	Leu	Asn	Glu	_	Gly 4270		Leu	Arg	Cys	His 4275	Cys	Trp	Pro
Ser	Tyr 4280	Ser	Gly	Glu	Arg	Cys 4285	Glu	Val	Asn	His	Cys 4290	Ser	Asn	Tyr
Cys	Gln 4295	Asn	Gly	Gly	Thr	Cys 4300	Val	Pro	Ser	Val	Leu 4305	Gly	Arg	Pro
Thr	Cys 4310	Ser	Cys	Ala	Leu	Gly 4315		Thr	Gly	Pro	Asn 4320	Cys	Gly	Lys
Thr	Val 4325	Cys	Glu	Asp	Phe	Cys 4330	Gln	Asn	Gly	Gly	Thr 4335	Cys	Ile	Val
Thr	Ala 4340	Gly	Asn	Gln	Pro	Tyr 4345	Cys	His	Cys	Gln	Pro 4350	Glu	Tyr	Thr
Gly	Asp 4355	Arg	Cys	Glń	Tyr	Tyr 4360		Cys	His	His	Tyr 4365	Cys	Val	Asn
Ser	Glu 4370	Ser	Cys	Thr	Ile	Gly 4375	Asp	Asp	Gly	Ser	Leu 4380	Glu	Cys	Val
Cys	Pro 4385	Thr	Arg	Tyr	Glu	Gly 4390	Pro	Lys	Cys	Glu	Val 4395		Lys	Cys
Val	Arg 4400	Cys	His	Gly	Gly	His 4405		Ile	Ile	Asn	Lys 4410	Asp	Ser	Glu
Asp	Ile 4415	Phe	Cys	Asn	Cys	Thr 4420	Asn	Gly	Lys	Ile	Ala 4425	Ser	Ser	Cys
Gln	Leu 4430	Cys	Asp	Gly	Tyr	Cys 4435	Tyr	Asn	Gly	Gly	Thr 4440	Cys	Gln	Leu
Asp	Pro 4445	Glu	Thr	Asn	Val	Pro 4450	Val	Cys	Leu	Cys	Ser 4455	Thr	Asn	Trp

Ser Gly Thr Gln Cys Glu Arg Pro Ala Pro Lys Ser Ser Lys Ser 4460 4465 Asp His Ile Ser Thr Arg Ser Ile Ala Ile Ile Val Pro Leu Val 4475 4480 4485 Leu Leu Val Thr Leu Ile Thr Thr Leu Val Ile Gly Leu Val Leu 4490 4495 Cys Lys Arg Lys Arg Arg Thr Lys Thr Ile Arg Arg Gln Pro Ile 4510 Ile Asn Gly Gly Ile Asn Val Glu Ile Gly Asn Pro Ser Tyr Asn Met Tyr Glu Val Asp His Asp His Asn Asp Gly Gly Leu Leu Asp 4535 4540 4545 Pro Gly Phe Met Ile Asp Pro Thr Lys Ala Arg Tyr Ile Gly Gly 4550 4555 4560 Gly Pro Ser Ala Phe Lys Leu Pro His Thr Ala Pro Pro Ile Tyr 4565 4570 4575 Leu Asn Ser Asp Leu Lys Gly Pro Leu Thr Ala Gly Pro Thr Asn 4585 4580 Tyr Ser Asn Pro Val Tyr Ala Lys Leu Tyr Met Asp Gly Gln Asn 4595 4600 4605 Cys Arg Asn Ser Leu Gly Ser Val Asp Glu Arg Lys Glu Leu Leu 4610 Pro Lys Lys Ile Glu Ile Gly Ile Arg Glu Thr Val Ala 4625 4630 <210> 34 <211> 2242 <212> DNA <213> Homo sapiens <220> <221> misc feature <223> n = \overline{a} or c or g or t <400> 34 gaatgccttt tagtgccttg cttcctgaac tagctcacag tagcccggcg gcccagggca

atccgaccac atttcactct caccgctgta ggaatccaga tgcaggccaa gtacagcagc

60

120

acgagggaca	tgctggatga	tgatggggac	accaccatga	gcctgcattc	tcaagcctct	180
gccacaactc	ggcatccaga	gccccggcgc	acagagcaca	gggctccctc	ttcaacgtgg	240
cgaccagtgg	ccctgaccct	gctgactttg	tgcttggtgc	tgctgatagg	gctggcagcc	300
ctggggcttt	tgttttttca	gtactaccag	ctctccaata	ctggtcaaga	caccatttct	360
caaatggaag	aaagattagg	aaatacgtcc	caagagttgc	aatctcttca	agtccagaat	420
ataaagcttg	caggaagtct	gcagcatgtg	gctgaaaaac	tctgtcgtga	gctgtataac	480
aaagctggag	cacacaggtg	cagcccttgt	acagaacaat	ggaaatggca	tggagacaat	540
tgctaccagt	tctataaaga	cagcaaaagt	tgggaggact	gtaaatattt	ctgccttagt	600
gaaaactcta	ccatgctgaa	gataaacaaa	caagaagacc	tggaatttgc	cgcgtctcag	660
agctactctg	agtttttcta	ctcttattgg	acagggcttt	tgcgccctga	cagtggcaag	720
gcctggctgt	ggatggatgg	aacccctttc	acttetgaac	tgttccatat	tataatagat	780
gtcaccagcc	caagaagcag	agactgtgtg	gccatcctta	atgggatgat	cttctcaaag	840
gactgcaaag	aattgaagcg	ttgtgtctgt	gagagaaggg	caggaatggt	gaagccagag	900
agcctccatg	tcccccctga	aacattaggc	gaaggtgact	gattcgccct	ctgcaactac	960
aaatagcaga	gtgagccagg	cggtgccaaa	gcaagggcta	gttgagacat	tgggaaatgg	1020
aacataatca	ggaaagacta	tctctctgac	tagtacaaaa	tgggttctcg	tgtttcctgt	1080
tcaggatcac	cagcatttct	gagcttgggt	ttatgcacgt	atttaacagt	cacaagaagt	1140
cttatttaca	tgccaccaac	caacctcaga	aacccataat	gtcatctgcc	ttcttggctt	1200
agagataact	tttagctctc	tttcttctca	atgtctaata	tcacctccct	gttttcatgt	1260
cttccttaca	cttggtggaa	taagaaactt	tttgaagtag	aggaaataca	ttgaggtaac	1320
atccttttct	ctgacagtca	agtagtccat	cagaaattgg	cagtcacttc	ccagattgta	1380
ccagcaaata	cacaaggaat	tctttttgtt	tgtttcagtt	catactagtc	ccttcccaat	1440
ccatcagtaa	agaccccatc	tgccttgtcc	atgccgtttc	ccaacaggga	tgtcacttga	1500
tatgagaatc	tcaaatctca	atgccttata	agcattcctt	cctgtgtcca	ttaagactct	1560
gataattgtc	tcccctccat	aggaatttct	cccaggaaag	aaatatatcc	ccatctccgt	1620
ttcatatcag	aactaccgtc	cccgatattc	ccttcagaga	gattaaagac	cagaaaaaag	1680
tgagcctctt	catctgcacc	tgtaatagtt	tcagttccta	ttttcttcca	ttgacccata	1740
tttatacctt	tcaggtactg	aagatttaat	aataataaat	gtaaatactg	tgaagtgtgt	1800
gtgattttac	aatggactta	tggttggtgg	gaaaattcag	catggaaatg	cttttcaaaa	1860
tatgatagcg	gtcattattt	tgattgtgcc	ttactgaaag	tttttgggga	atttacaaga	1920
gtactgatta	catgattatc	tggagaaaat	aagatgtctt	tgaaatacat	gttggcttca	1980
agaaaacagt	tttaacgttt	tcctaaaatg	aaatcttttg	aggtgagctt	atggcatcaa	2040

cacatggttg	atgaggaagc	tgagttgcat	tagtgcacat	gatttccagt	caggtcatgg	2100
gaaatgaaca	gagacagtga	catctttgta	gctgctcctt	tgtgaggcac	ttctttcttg	2160
agatgactcc	atgcacaaat	ataacaggga	tcattgggaa	tgacaccatc	acagccacca	2220
agnttattgg	gttactgata	at				2242

<210> 35

<211> 280

<212> PRT

<213> Homo sapiens

<400> 35

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His 20 25 30

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg 35 40 45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly 50 55 60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn 65 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr 85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly 100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys 115 120 125

Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His 130 135 140

Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp 145 150 155 160

Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn
165 170 175

Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe 180 185 190

Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala 195 200 205

Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile 210 215 220

Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu 225 230 235 240

Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val 245 250 255 Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro 260 265 270

Pro Glu Thr Leu Gly Glu Gly Asp 275 280

<210> 36

<211> 2323

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

 $\langle 223 \rangle$ n = a or c or g or t

<400> 36 gaatgccttt tagtgccttg cttcctgaac tagctcacag tagcccggcg gcccagggca 60 atcogaccac atttcactct caccgctgta ggaatccaga tgcaggccaa gtacagcagc 120 acqaqqqaca tqctqqatqa tqatqqqqac accaccatqa qcctqcattc tcaagcctct 180 gccacaactc ggcatccaga gccccggcgc acagagcaca gggctccctc ttcaacgtgg 240 cqaccaqtqq ccctqaccct qctqactttq tqcttqqtqc tqctgatagg gctggcagcc 300 ctggggettt Egtttttca gtactaccag etetecaata etggteaaga caecatttet 360 caaatggaag aaagattagg aaatacgtcc caagagttgc aatctcttca agtccagaat 420 ataaagettg caggaagtet geageatgtg getgaaaaac tetgtegtga getgtataac 480 aaaqetqqaq qetatacaaq aaacatqqtq ccagcatetq ettettetga gageetcagg 540 cagettecae acatggggga aagtgeagea geacaeaggt geagecettg tacagaacaa 600 tggaaatggc atggagacaa ttgctaccag ttctataaag acagcaaaag ttgggaggac 660 720 tgtaaatatt totgoottag tgaaaactot accatgotga agataaacaa acaagaagac ctggaatttg ccgcgtctca gagctactct gagtttttct actcttattg gacagggctt 780 840 ttgcgccctg acagtggcaa ggcctggctg tggatggatg gaaccccttt cacttctgaa ctgttccata ttataataga tgtcaccagc ccaagaagca gagactgtgt ggccatcctt 900 aatgggatga tetteteaaa ggaetgeaaa gaattgaage gttgtgtetg tgagagaagg 960 gcaggaatgg tgaagccaga gagcctccat gtccccctg aaacattagg cgaaggtgac 1020 tgattcgccc tctgcaacta caaatagcag agtgagccag gcggtgccaa agcaagggct 1080 agttqaqaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtacaaa 1140 atgggttete gtgttteetg tteaggatea ceageattte tgagettggg tttatgeaeg 1200 tatttaacag tcacaagaag tcttatttac atgccaccaa ccaacctcag aaacccataa 1260 tgtcatctgc cttcttggct tagagataac ttttagctct ctttcttctc aatgtctaat 1320 atcacctccc tgttttcatg tcttccttac acttggtgga ataagaaact ttttgaagta 1380

gaggaaatac	attgaggtaa	catccttttc	tctgacagtc	aagtagtcca	tcagaaattg	1440
gcagtcactt	cccagattgt	accagcaaat	acacaaggaa	ttctttttgt	ttgtttcagt	1500
tcatactagt	cccttcccaa	tccatcagta	aagaccccat	ctgccttgtc	catgccgttt	1560
cccaacaggg	atgtcacttg	atatgagaat	ctcaaatctc	aatgccttat	aagcattcct	1620
tcctgtgtcc	attaagactc	tgataattgt	ctcccctcca	taggaatttc	tcccaggaaa	1680
gaaatatatc	cccatctccg	tttcatatca	gaactaccgt	ccccgatatt	cccttcagag	1740
agattaaaga	ccagaaaaaa	gtgagcctct	tcatctgcac	ctgtaatagt	ttcagttcct	1800
attttcttcc	attgacccat	atttatacct	ttcaggtact	gaagatttaa	taataataaa	1860
tgtaaatact	gtgaagtgtg	tgtgatttta	caatggactt	atggttggtg	ggaaaattca	1920
gcatggaaat	gcttttcaaa	atatgatagc	ggtcattatt	ttgattgtgc	cttactgaaa	1980
gtttttgggg	aatttacaag	agtactgatt	acatgattat	ctggagaaaa	taagatgtct	2040
ttgaaataca	tgttggcttc	aagaaaacag	ttttaacgtt	ttcctaaaat	gaaatctttt	2100
gaggtgagct	tatggcatca	acacatggtt	gatgaggaag	ctgagttgca	ttagtgcaca	2160
tgatttccag	tcaggtcatg	ggaaatgaac	agagacagtg	acatctttgt	agctgctcct	2220
ttgtgaggca	cttctttctt	gagatgactc	catgcacaaa	tataacaggg	atcattggga	2280
atgacaccat	cacagccacc	aagnttattg	ggttactgat	aat		2323

<210> 37 <211> 307 <212> PRT <213> Homo sapiens

<400> 37

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Gly 1 10 15

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His 20 25 30

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg 35 40 45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly 50 60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn 65 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr 85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys 115 120 125

Ala Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu 130 135 140	
Ser Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg 145 150 155 160	
Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr 165 170 175	
Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys 180 185 190	
Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu 195 200 205	
Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp 210 215 220	
Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp 225 230 235 240	
Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr 245 250 . 255	
Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe 260 265 270	
Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala 275 280 285	
Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly 290 295 300	
Glu Gly Asp 305	
<210> 38 <211> 2714	
<212> DNA <213> Homo sapiens	
<400> 38 capacidades de la companya del companya del companya de la companya del companya de la companya del companya de la companya del companya de la companya del companya de la compan	g 60
atttegtegg gaggaatgga aggagaagge ggaatgtggg agggeteagg gggatgtgg	ıg 120
agggacgaac ggagaagggg gagagagggg ggtccagtct cccctggccg agcattttt	t 180
ttttggaagt octaggactg atctccagga ccagcactct tctcccagcc cttagggtc	c 240
tgctcggcca aggccttccc tgccatgcga cctgtcagtg tctggcagtg gagcccctg	ıg 300
gggctgctgc tgtgcctgct gtgcagttcg tgcttggggt ctccgtcccc ttccacggg	JC 360
cctgagaaga aggccgggag ccaggggctt cggttccggc tggctggctt ccccaggaa	ig 420
ccctacgagg gccgcgtgga gatacagcga gctggtgaat ggggcaccat ctgcgatga	it 480
gacttcacgc tgcaggctgc ccacatcctc tgccgggagc tgggcttcac agaggccac	:a 540
ggctggaccc acagtgccaa atatggccct ggaacaggcc gcatctggct ggacaactt	g 600
agctgcagtg ggaccgagca gagtgtgact gaatgtgcct cccggggctg ggggaacag	jt 660

gactgtacgc	acgatgagga	tgctggggtc	atctgcaaag	accagcgcct	ccctggcttc	720
tcggactcca	atgtcattga	ggtagagcat	cacctgcaag	tggaggaggt	gcgaattcga	780
cccgccgttg	ggtggggcag	acgacccctg	cccgtgacgg	aggggctggt	ggaagtcagg	840
cttcctgacg	gctggtcgca	agtgtgcgac	aaaggctgga	gcgcccacaa	cagccacgtg	900
gtctgcggga	tgctgggctt	ccccagcgaa	aagagggtca	acgcggcctt	ctacagaaag	960
ttgaggaagc	gagcggccaa	ggtctcagcc	cgacacccca	agccccttgg	aaggctgcta	1020
gcccaacggc	agcaacactc	ctttggtctg	catggggtgg	cgtgcgtggg	cacggaggcc	1080
cacctctccc	tetgtteect	ggagttctat	cgtgccaatg	acaccgccag	gtgccctggg	1140
gggggccctg	cagtggtgag	ctgtgtgcca	ggccctgtct	acgcggcatc	cagtggccag	1200
aagaagcaac	aacagtcgaa	gcctcagggg	gaggcccgtg	tccgtctaaa	gggcggcgcc	1260
caccctggag	agggccgggt	agaagtcctg	aaggccagca	catggggcac	agtctgtgac	1320
cgcaagtggg	acctgcatgc	agccagcgtg	gtgtgtcggg	agctgggctt	cgggagtgct	1380
cgagaagctc	tgagtggcgc	tcgcatgggg	cagggcatgg	gtgctatcca	cctgagtgaa	1440
gttcgctgct	ctggacagga	getetecete	tggaagtgcc	cccacaagaa	catcacagct	1500
gaggattgtt	cacatagcca	ggatgccggg	gtccggtgca	acctacctta	cactggggca	1560
gagaccagga	tccgactcag	tgggggccgc	agccaacatg	aggggcgagt	cgaggtgcaa	1620
atagggggac	ctgggcccct	tegetgggge	ctcatctgtg	gggatgactg	ggggaccctg	1680
gaggccatgg	tggcctgtag	gcaactgggt	ctgggctacg	ccaaccacgg	cctgcaggag	1740
acctggtact	gggactctgg	gaatataaca	gaggtggtga	tgagtggagt	gcgctgcaca	1800
gggactgagc	tgtccctgga	tcagtgtgcc	catcatggca	cccacatcac	ctgcaagagg	1860
acagggaccc	gcttcactgc	tggagtcatc	tgttctgaga	ctgcatcaga	tctgttgctg	1920
cactcagcac	tggtgcagga	gaccgcctac	atcgaagacc	ggcccctgca	tatgttgtac	1980
tgtgctgcgg	aagagaactg	cctggccagc	tcagcccgct	cagccaactg	gccctatggt	2040
caccggcgtc	tgctccgatt	ctcctcccag	atccacaacc	tgggacgagc	tgacttcagg	2100
cccaaggctg	ggcgccactc	ctgggtgtgg	cacgagtgcc	atgggcatta	ccacagcatg	2160
gacatcttca	ctcactatga	tatcctcacc	ccaaatggca	ccaaggtggc	tgagggccac	2220
aaagctagtt	tctgtctcga	agacactgag	tgtcaggagg	atgtctccaa	gcggtatgag	2280
tgtgccaact	ttggagagca	aggcatcact	gtgggttgct	gggatctcta	ccggcatgac	2340
attgactgtc	agtggattga	catcacggat	gtgaagccag	gaaactacat	tctccaggtt	2400
gtcatcaacc	caaactttga	agtagcagag	agtgacttta	ccaacaatgc	aatgaaatgt	2460
aactgcaaat	atgatggaca	tagaatctgg	gtgcacaact	gccacattgg	tgatgccttc	2520
agtgaagagg	cccacaggag	gtttgaacgc	teccetggee	agaccagcac	ctagattatg	2580

taagtgccac tgccctttgc aaaccgcccc tggcgcctaa tggcaggggt ctgaggctgc	2640
cattacetea ggagettate aagaaaceea tgteageaae catgtattge ggeegeteta	2700
gaggaatege cage	2714
<210> 39 <211> 769 <212> PRT <213> Homo sapiens	·
<400> 39	
Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu 1 5 10 15	
Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly 20 25 30	
Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly 35 40 45	
Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly 50 55 60	
Glu Trp Gly Thr Ile Cys Asp Asp Phe Thr Leu Gln Ala Ala His 65 70 75 80	
Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His 85 90 95	
Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu 100 105 110	
Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly 115 120 . 125	
Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys 130 135 140	
Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val 145 150 155 160	
Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly 165 170 175	
Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg 180 185 190	
Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His 195 200 205	
Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg 210 215 220	
Val Asn Ala Ala Phe Tyr Arg Lys Leu Arg Lys Arg Ala Ala Lys Val 225 230 235 240	
Ser Ala Arg His Pro Lys Pro Leu Gly Arg Leu Leu Ala Gln Arg Gln 245 250 255	
Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala	

270 260 265 His Leu Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala 280 Arg Cys Pro Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro 310 Gln Gly Glu Ala Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp 345 Arg Lys Trp Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly 360 Phe Gly Ser Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu 390 Ser Leu Trp Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala 425 Glu Thr Arg Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg 440 435 Val Glu Val Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln 475 470 Leu Gly Leu Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr 505 Gly Thr Glu Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile 520 Thr Cys Lys Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala Ser Asp Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu 565 Glu Asn Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly 585 His Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg

Ala	Asp 610	Phe	Arg	Pro	Lys	Ala 615	Gly	Arg	His	Ser	Trp 620	Val	Trp	His	Glu		
Cys 625	His	Gly	His	Tyr	His 630	Ser	Met	Asp	Ile	Phe 635	Thr	His	Tyr	Asp	Ile 640		
Leu	Thr	Pro	Asn	Gly 645	Thr	Lys	Val	Ala	Glu 650	Gly	His	Lys	Ala	Ser 655	Phe		
Cys	Leu	Glu	Asp 660	Thr	Glu	Cys	Gln	Glu 665	Asp	Val	Ser	Lys	Arg 670	Tyr	Glu		
Cys	Ala	Asn 675	Phe	Gly	Glu	Gln	Gly 680	Ile	Thr	Val	Gly	Cys 685	Trp	Asp	Leu		
Tyr	Arg 690	His	Asp	Ile	Asp	Cys 695	Gln	Trp	Ile	Asp	Ile 700	Thr	Asp	Val	Lys		
Pro 705	Gly	Asn	Tyr	Ile	Leu 710	Gln	Val	Val	Ile	Asn 715	Pro	Asn	Phe	Glu	Val 720		
Ala	Glu	Ser	Asp	Phe 725	Thr	Asn	Asn	Ala	Met 730	Lys	Cys	Asn	Сув	Lys 735	Tyr		
Asp	Gly	His	Arg 740	Ile	Trp	Val	His	Asn 745	Cys	His	Ile	Gly	Asp 750	Ala	Phe		
Ser	Glu	Glu 755	Ala	His	Arg	Arg	Phe 760	Glu	Arg	Ser	Pro	Gly 765	Gln	Thr	Ser		
Thr																	
<210		10													•		
<213 <213	2 > I	1877 ONA															
<213			sapi	lens													
<400 gtag		tg	tgcaa	aaaca	at ac	ctagt	eggat	ata	agaga	atga	ataa	agaaa	aaa 🤉	gccc	tgcac		60
tcaa	aaga	gct (ctcgg	gatto	a to	caaca	aaatt	ati	tgtg	cagt	taga	atago	cct (cecto	cacct	:	120
gtct	tct	cag a	agcag	ggtaa	at go	gcaag	gcato	g gct	gccg	gtgc	tcad	cctg	ggc 1	tetg	gctctt		180
cttt	cago	gt	tttc	ggcca	ac co	caggo	cacgo	g aa	aggct	tct	ggga	acta	ctt (cagco	cagacc	:	240
agc	9999	aca a	aaggo	caggg	gt gg	gagca	agato	c cat	cago	caga	agat	ggct	cg (cgago	ccgcg	:	300
acco	ctgaa	aag	acago	cctt	ga go	caaga	accto	c aa	caata	atga	acaa	agtto	cct (ggaaa	agctg	:	360
aggo	cctc	cga (gtgg	gagc	ga go	gete	ctcgg	g ct	ccca	cagg	acco	ggt	9 9 9 (catgo	eggegg		420
cago	ctgc	agg i	aggag	gttgg	ga go	gaggt	tgaag	g gc	cgc	ctcc	agco	ccta	cat o	ggcag	gaggcg		480
cac	gagci	tgg	tggg	ctgga	aa t	tgga	agggo	e tt	gcgg	cagc	aact	gaag	gcc (ctaca	acgatg	!	540

gatctgatgg agcaggtggc cctgcgcgtg caggagctgc aggagcagtt gcgcgtggtg

ggggaagaca ccaaggccca gttgctgggg ggcgtggacg aggcttgggc tttgctgcag

720 ggactgcaga gccgcgtggt gcaccacacc ggccgcttca aagagctctt ccacccatac 780 gccgagagcc tggtgagcgg catcgggcgc cacgtgcagg agctgcaccg cagtgtggct 840 ccgcacgccc ccgccagccc cgcgcgcctc agtcgctgcg tgcaggtgct ctcccggaag ctcacgctca aggccaaggc cctgcacgca cgcatccagc agaacctgga ccagctgcgc 900 gaagagetea geagageett tgeaggeact gggaetgagg aaggggeegg eeeggaeeee 960 cagatgetet eegaggaggt gegeeagega etteaggett teegeeagga eacetaeetg 1020 1080 cagatagetg cetteacteg egecategae caggagactg aggaggteca geageagetg gegecacete caccaggeca cagtgeette gecccagagt tteaacaaac agacagtgge 1140 aaggttetga geaagetgea ggeeegtetg gatgaeetgt gggaagaeat eacteaeage 1200 cttcatgacc agggccacag ccatctgggg gacccctgag gatctacctg cccaggccca 1260 ttcccagctc cttgtctggg gagccttggc tctgagcctc tagcatggtt cagtccttga 1320 aagtggcctg ttgggtggag ggtggaaggt cctgtgcagg acagggaggc caccaaaggg 1380 getgetgtet cetgeacate cagecteetg egacteecca atetggatge attacattea 1440 ccaggetttg caaacccage etcecagtge teatttggga atgeteatga gttactccat 1500 tcaagggtga gggagtaggg agggagaggc accatgcatg tgggtgatta tctgcaagcc 1560 tgtttgccgt gatgctggaa gcctgtgcca ctacatcctg gagtctgaca ctgagcccct 1620 gcgagtgacc gtgagcacac agttccgtag cggggcccat acgagactcg acgcgcgcgc 1680 accacgaggt cccgagggag gacactcgac ggacacgagt gacgggaaat gtgcatctac 1740 actagogogo gacagotaga gogatgacgg egaggacgto togcagocta coagcaacgo 1800 gaagacgtgc ctcccggcgt cgtatggatt aacaagctcc aagtagggtg tacaacgccg 1860 1877 cagcatgaac tcccagg

```
<210> 41
```

Met Asn Lys Lys Pro Leu His Ser Lys Ser Ser Arg Ile His Gln
1 5 10 15

Gln Ile Ile Val Gln Leu Asp Ser Leu Pro Pro Pro Val Phe Ser Glu 20 25 30

Gln Val Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala Leu Ala Leu 35 40 45

Leu Ser Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr 50 55

Phe Ser Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln

<211> 400

<212> PRT

<213> Homo sapiens

<400> 41

75 65 Gln Lys Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser 105 Gly Ser Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg 120 Gln Leu Gln Glu Glu Leu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg 150 155 Gln Gln Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala Leu Leu Gln 200 Gly Leu Gln Ser Arg Val Val His His Thr Gly Arg Phe Lys Glu Leu Phe His Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu Leu His Arg Ser Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg 280 Glu Glu Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Gly Pro Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala 330 Ile Asp Gln Glu Thr Glu Glu Val Gln Gln Leu Ala Pro Pro Pro 345 Pro Gly His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp 375 Ile Thr His Ser Leu His Asp Gln Gly His Ser His Leu Gly Asp Pro <210> 42

<211> 2128

<212> DNA <213> Homo sapiens

<400> 42 geaceggice ggaalteeeg ggiegaegat tiegteteaa eatteageag aggeeeeaga 60 tragregation agreeaggers areastgares aggaggatigg gatrotigggt gragetrate 120 180 acaagcgtcg gggtgcagca aaaccatcca ggctggacag tggctggaca gttccaagaa aagaaacgct tcactgaaga agtcattgaa tacttccaga agaaagttag cccagtgcat 240 300 ctgaaaatcc tgctgactag cgatgaagcc tggaagagat ttgtgcgtgt ggctgaattg 360 cccagggaag aggcagatgc tctctatgaa gctctgaaga atcttacacc atatgtgact attgaggaca aagacatgca gcaaaaagaa cagcagttta gggagtggtt tttgaaagag 420 480 tttcctcaaa tcagatggaa gattcaggag tccatagaaa ggcttcgtgt cattgcaaat gagattgaaa aggtccacag aggctgcgtc atcgccaatg tggtgtctgg ctccactggc 540 600 atcctgtctg tcattggcgt tatgttggca ccatttacag cagggctgag cctgagcatt actgcagetg gggtaggget gggaatagea tetgecaegg etgggatege etccageate 660 720 gtggagaaca catacacaag gtcagcagaa ctcacagcca gcaggctgac tgcaaccagc actgaccaat tggaggcatt aagggacatt ctgcatgaca tcacacccaa tgtgctttcc 780 tttgcacttg attttgacga agccacaaaa atgattgcga atgatgtcca tacactcagg 840 agatotaaag ccactgttgg acgoootttg attgottggo gatatgtaco tataaatgtt 900 960 gttgagacac tgagaacacg tggggccccc acccggatag tgagaaaagt agcccggaac ctgggcaagg ccacttcagg tgtccttgtt gtgctggatg tagtcaacct tgtgcaagac 1020 tcactggact tgcacaaggg ggcaaaatcc gagtctgctg agtcgctgag gcagtgggct 1080 caggagetgg aggagaatet caatgagete acceatatee ateagagtet aaaagcagge 1140 1200 taggcccaat tgttgcggga agtcagggac cccaaacgga gggactggct gaagccatgg cagaagaacg tggattgtga agatttcatg gacatttatt agttccccaa attaatactt 1260 ttataattto ctatgootgt otttacogoa atototaaac acaaattgtg aagatttoat 1320 1380 atctcctaat cctgtcagct gaggaggatg tatgtcacct caggaccatg tgataattgc 1440 gttaactgca caaattgtag agcatgtgtg tttgaacaat atgaaatctg ggcaccttga 1500 aaaaagaaca ggataacagc aattgttcag ggaataagag agataacctt aaactctgac 1560 caacagtgag ccgggtggaa cagagtcata tttctcttct ttcaaaagca aatgggagaa 1620 atatogotga attottttto toagoaagga acatoootga gaaagagaat goacoootga 1680

gggtgggtct ataaatggcc tccttgggtg tggccatctt ctatggtcga gactgtaggg

1740

a	tgaaataaa	ccccagtctc	ccatagtgct	cccaggctta	ttaggaagag	gaaattcccg	1800
С	ctaataaat	tttggtcaga	ccggttgctc	tcaaaaccct	gtctcctgat	aagatgttat	1860
С	aatgacaat	ggtgcctgaa	acctcattag	caattttaat	ttctccccgg	tectgtggte	1920
С	tgtgatctc	accctgcctc	cacttgcctt	gtgatattct	attaccttgt	gaagtaggtg	1980
a	tctttgtga	cccacaccct	attcatacac	tccctcccct	tttgaaagtc	cctaataaaa	2040
а	cttgctggt	tttgcagctt	gtgaggcatc	acggaaccta	ctgatgtgtg	atgtctcccc	2100
t	ggacaccta	gctttaaaat	ttcaaaaa				2128

<210> 43 <211> 348

<212> PRT

<213> Homo sapiens

<400> 43

Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn 1 5 10

His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe 20 25 30

Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His 35 40 45

Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg 50 55 60

Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu 65 . 70 75 80

Lys Asn Leu Thr Pro Tyr Val Thr Ile Glu Asp Lys Asp Met Gln Gln 85 90 95

Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile 100 105 110

Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn 115 120 125

Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser 130 135 140

Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe 145 150 150 160

Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly 165 170 175

Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr

Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser 195 200 205

Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro 210 215 220

Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile 225 230 235 240											
Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg 245 250 255											
Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu 260 265 270											
Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn 275 280 285											
Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn 290 295 300											
Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser 305 310 315 320											
Ala Glu Ser Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn 325 330 335											
Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly 340 345											
<210> 44 <211> 988 <212> DNA <213> Homo sapiens											
<220> <221> misc_feature <223> n = a or c or g or t											
<220> <221> CDS <222> (129)(971)											
<400> 44 agagetgeeg gngnnnnaat ggatagaata etettgaeea nngaegeaeg ageetgaaet	60										
ageteacagt ageceggegg eccagggeaa teegaceaca titeactete accgetgtag	120										
gaatccag atg cag gcc aag tac agc agc acg agg gac atg ctg gat gat Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp 1 5 10	170										
gat ggg gac acc acc atg agc ctg cat tct caa gcc tct gcc aca act Asp Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr 15 20 25 30	218										
cgg cat cca gag ccc cgg cgc aca gtt ttt cag tac tac cag ctc tcc Arg His Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser 35 40 45	266										
aat act ggt caa gac acc att tct caa atg gaa gaa aga tta gga aat Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn 50 55 60	314										
acg tcc caa gag ttg caa tct ctt caa gtc cag aat ata aag ctt gca	362										

	~ ~	_	_	_		 _	_			_	_		-	tat Tyr		410
														tct Ser		458
														gca Ala 125		506
														aat Asn		554
														tat Tyr		602
														gaa Glu		650
Harry Jun Harly Harry	-	~				_	-							tct Ser		698
til Hall Hen Hen i														tgg Trp 205		746
the first the state of the stat														gat Asp		794
														atg Met		842
			_	_		_	_	_	_	_		_		aga Arg	-	890
														aca Thr		938
					atg Met 275						tago	cctag	ggt t	ctag	gac	988

<210> 45

<211> 281 <212> PRT

<213> Homo sapiens

<220>

<221> misc_feature <223> n = a or c or g or t

<400> 45

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly 1 10 15

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His 20 25 30

Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser Asn Thr 35 40 45

Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser 50 60

Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser 65 70 75 80

Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala 85 90 95

Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser 100 105 110

Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys 115 120 125

Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln 130 135 140

Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu 165 170 . 175

Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr 180 185 190

Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly 195 200 205

Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser 210 215 220

Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser 225 230 235

Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly 245 250 250

Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu 260 265 270

Gly Asp Met His His His His His 275